

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2003, 15:33:20 : Search time 11456 Seconds
(without alignments)
11612.963 Million cell updates/sec

Title: us-09-965-830-1_COPY_6_3257
Perfect score: 3252
Sequence: 1 atgcgcgcacatgcgggcct.....aagaagcacacaggggtctga 3252

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 9
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg_hum.*
- 31: em.htg_inv.*
- 32: em.htg_other.*
- 33: em.htg_mus.*
- 34: em.htg_pla.*
- 35: em.htg_rod.*
- 36: em.htg_mam.*
- 37: em.htg_vit.*
- 38: em.sy.*
- 39: em.htgo_hum.*
- 40: em.htgo_mus.*
- 41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB	ID	Description
1	3252	100.0	3323	6	AR179189	AR179189 Sequence
2	3252	100.0	3610	9	AB022696	AB022696 Homo sapi
3	3250.4	100.0	3853	9	AB033108	AB033108 Homo sapi
4	3245.8	99.8	3249	6	AR217183	AR217183 Sequence
5	3244	99.8	3252	6	AX027893	AX027893 Sequence
6	3218	99.0	3857	6	AR212361	AR212361 Sequence
7	3156	97.0	3355	6	AR281263	AR281263 Sequence
8	3153	97.0	3249	6	AR281264	AR281264 Sequence
9	2664.8	81.9	3595	10	RN07627	AJ007627 Rattus no
10	2664.8	81.9	3715	6	AR179195	AR179195 Sequence
11	2664.8	81.9	3715	10	AB022697	AB022697 Rattus no
12	2660.8	81.8	3615	10	AF109143	AF109143 Mus muscu
13	1055.4	32.5	1432	9	BC033141	BC033141 Homo sapi
14	884.8	27.2	3264	6	AR179192	AR179192 Sequence
15	884.8	27.2	3420	9	AB022698	AB022698 Homo sapi
16	869.8	26.7	3688	10	RN07628	AJ007628 Rattus no
17	869.8	26.7	3736	6	AR179196	AR179196 Sequence
18	869.8	26.7	3736	10	AB022699	AB022699 Rattus no
19	844.4	26.0	870	6	AR281268	AR281268 Sequence
20	844.4	26.0	1132	6	AR281267	AR281267 Sequence
21	803.2	24.7	3743	10	AF061957	AF061957 Rattus no
22	761.2	23.4	3321	6	AR281271	AR281271 Sequence
23	761.2	23.4	5107	6	AR281270	AR281270 Sequence
24	761.2	23.4	5107	9	AY053503	AY053503 Homo sapi
25	601	18.5	161895	2	AC079849	AC079849 Homo sapi
26	601	18.5	186011	2	AC079451	AC079451 Homo sapi
27	601	18.5	188928	9	AC020612	AC020612 Homo sapi
28	572.8	17.6	1626	6	AR281266	AR281266 Sequence
29	572.8	17.6	2694	6	AR281265	AR281265 Sequence
30	572.8	17.6	5955	6	AR281269	AR281269 Sequence
31	541.6	16.7	3532	10	BC029690	BC029690 Mus muscu
32	479.2	14.7	209126	2	AC118646	AC118646 Mus muscu
33	479.2	14.7	259013	2	AC096892	AC096892 Rattus no
34	447.6	13.8	1059	10	RN07632	AJ007632 Rattus no
35	421.2	13.0	221470	2	AC027679	AC027679 Mus muscu
36	384	11.8	464	10	AF073892	AF073892 Rattus no
37	365.6	11.2	3352	9	AF311913	AF311913 Homo sapi
38	364.2	11.2	4263	3	DM004246	U34246 Drosophila
39	362.4	11.1	2877	6	AX686981	AX686981 Sequence
40	361.6	11.1	3405	4	BTEAG1	Y13430 Bos taurus
41	353.6	10.9	4569	10	RNPTGHS	U34264 R.norvegicu
42	349.2	10.7	3820	4	OCU87513	U87513 Oryctolagus
43	344.6	10.6	3486	4	BTEAG2	Y13431 Bos taurus
44	344.6	10.6	3480	9	AF363636	AF363636 Homo sapi
45	344.2	10.6	2477	9	HSA512214	AJ512214 Homo sapi

ALIGNMENTS

RESULT 1
AR179189
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES

AR179189
Sequence
AR179189
AR179189.1
GI:20220744
Unknown.
Unclassified.
1 (bases 1 to 3323)
Miyake,A., Mochizuki,S. and Yokoi,H.
Brain specific potassium channel protein
Patent: US 6326168-A 1 04-DEC-2001;
Location/Qualifiers

3323 bp
1 from patent US 6326168.
DNA
linear
FAT 20-APR-2002

2046	Db		AGCCTTGCGCTGTACCCCGAGTTTGCCCGCGCTTCAGTCTGTGGCTCCGAGGGAGCTC	2105
2101	Qy		AGCTACAAACCTGGGTGCTGGGCGAGGCTCTGCAGAGG*GGACACACAGCTCCCTGATCGGC	2160
2106	Db		AGCTACACCTTGGTGTCTGGGCGAGGCTCTGCAGAGGTGGACACCACTCCCTGAGGGGC	2165
2161	Qy		GACAATACCTTATGTCTCCAGCTGGAGGAGAGGAGACAGATGGGGAGCAGGCCGCAAG	2220
2166	Db		GACAATACCTTATGTCTCCAGCTGGAGGAGAGGAGACAGATGGGGAGCAGGCCGCCAGC	2225
2221	Qy		GTCTCCCGACCCGAGCTGATGAGCCCTCCAGCCCTTGCTGTCCCTGGCTGCACCTCC	2280
2226	Db		GTCTCCCGACCCGAGCTGATGAGCCCTCCAGCCCTTGCTGTCCCTGGCTGCACCTCC	2285
2281	Qy		TCATCTTCAGCTGCCAAGCTGTCTATCCCAAGCTCGAACACACCCCGGCTCTGCTTAGT	2340
2286	Db		TCATCTTCAGCTGCCAAGCTGTCTATCCCAAGCTCGAACACACCCCGGCTCTGCTTAGT	2345
2341	Qy		GGCAGAGGAGCCAGCAGGGGAGGGGCTTTGAGGGCTGAGGCTGGCCCTCTGCTCC	2400
2346	Db		GGCAGAGGAGCCAGCAGGGGAGGGGCTTTGAGGGCTGAGGCTGGCCCTCTGCTCC	2405
2401	Qy		CCACGGGCCCTAGAGGGGCTACGGCTGCCCCCATGCCATGGAATGTGCCGCCACAG*CTG	2460
2406	Db		CCACGGGCCCTAGAGGGGCTACGGCTGCCCCCATGCCATGGAATGTGCCGCCACAG*CTG	2465
2461	Qy		AGCCCCAGGCTAGATGGATTGAAGACGGCTGTGGCTGGAGCAACCCCAAGCTCTCT	2520
2466	Db		AGCCCCAGGCTAGTAGATGGATTGAAGACGGCTGTGGCTGGAGCAACCCCAAGCTCTCT	2525
2521	Qy		TTCCGCTGGGCCAGTCTGGCCCGGAATGTAGCAGACGCCCTCCCTGSGACCAGAGC	2580
2526	Db		TTCCGCTGGGCCAGTCTGGCCCGGAATGTAGCAGACGCCCTCCCTGSGACCAGAGC	2585
2581	Qy		GGCTGCTCACTGTCTCCCATGGCCCCAGGAGCAAGGAACACAGACACACTGGACAAG	2640
2586	Db		GGCTGCTCACTGTCTCCCATGGCCCCAGGAGCAAGGAACACAGACACACTGGACAAG	2645
2641	Qy		CTTGCGCAGGGCGCTCAGAGAGCTCTCAGACAGGTGCTCAGATGGGGAAGACTCGAG	2700
2646	Db		CTTGCGCAGGGCGTACAGAGCTCTCAGACAGGTGCTCAGATGGGGAAGACTCGAG	2705
2701	Qy		TCACTTCGCTAGGCTGTGACCTTGTCTGGGCCGCCACAGGAGGGTCCGTGGCCCTCG	2760
2706	Db		TCACTTCGCTAGGCTGTGACCTTGTCTGGGCCGCCACAGGAGGGTCCGTGGCCCTCG	2765
2761	Qy		GCATCGGAGAGGGCGCTGCCAGCCAGCACCTCCGGGCTTCTGCACGCTCTGTGTGTG	2820
2766	Db		GCATCGGAGAGGGCGCTGCCAGCCAGCACCTCCGGGCTTCTGCACGCTCTGTGTGTG	2825
2821	Qy		GACACTGGGCGATCTCTTACTGCTCAGGCCGCCAGCTGGCTGTGCTTGAGTGGGACT	2880
2826	Db		GACACTGGGCGATCTCTTACTGCTCAGGCCGCCAGCTGGCTGTGCTTGAGTGGGACT	2885
2881	Qy		TGGCCCCACCTCTCGGGGGCTCTCCCTCATGGCACCTCGGCCCTGGGCTGGGCTCCGCA	2940
2886	Db		TGGCCCCACCTCTCGGGGGCTCTCCCTCATGGCACCTCGGCCCTGGGCTGGGCTCCGCA	2945
2941	Qy		GGGTCTCAGAGCTCCCTCTGGCTCTGAGGCCACAGCTTTCTGAGACCTCCACCTCAGACTCA	3000
2946	Db		GGGTCTCAGAGCTCCCTCTGGCTCTGAGGCCACAGCTTTCTGAGACCTCCACCTCAGACTCA	3005
3001	Qy		GAGCCCCCTGCTCAGGAGACTCTGCTCTGAGCCAGCACCCCTGCCCTCCCTCCTCT	3060
3006	Db		GAGCCCCCTGCTCAGGAGACTCTGCTCTGAGCCAGCACCCCTGCCCTCCCTCCTCT	3065
3061	Qy		CTTGAGGAAGGGGCTTAGACTTGGGCCCGCAGAGCCCTGTGAGCCAGGCTGAGGCTACCAAGC	3120
3066	Db		CTTGAGGAAGGGGCTTAGACTTGGGCCCGCAGAGCCCTGTGAGCCAGGCTGAGGCTACCAAGC	3125
3121	Qy		ACTGGAGGCCCCCAACAGGCTCAGGGGGCTTGGCTTGGCTGGGAGCCCAACAGGCTG	3180

126	3126	ACTTGAGAGCCCCACACAGGGTCAAGGGGCGCTGGCCCTTGGCCATGGGACACCCACACGCTG	3189	GAGATGGTGCTTATTTGGCTCCCATGCTCTGGCACAGTCCAGTGGAGCCAGGAAGGC	3240		3186	GAGATGGTGCTTATTTGGCTGCCATGCTCTGGCACAGTCCAGTGGAGCCAGGAAGGC	3245	
Qy	3181	GAGATGGTGCTTATTTGGCTCCCATGCTCTGGCACAGTCCAGTGGAGCCAGGAAGGC	3240		3189	GAGATGGTGCTTATTTGGCTCCCATGCTCTGGCACAGTCCAGTGGAGCCAGGAAGGC	3245		3186	GAGATGGTGCTTATTTGGCTGCCATGCTCTGGCACAGTCCAGTGGAGCCAGGAAGGC
Db	3186	GAGATGGTGCTTATTTGGCTGCCATGCTCTGGCACAGTCCAGTGGAGCCAGGAAGGC	3245		3189	GAGATGGTGCTTATTTGGCTCCCATGCTCTGGCACAGTCCAGTGGAGCCAGGAAGGC	3240		3181	GAGATGGTGCTTATTTGGCTCCCATGCTCTGGCACAGTCCAGTGGAGCCAGGAAGGC
Qy	3241	ACAGGGGTCTGA	3252		3189	GAGATGGTGCTTATTTGGCTCCCATGCTCTGGCACAGTCCAGTGGAGCCAGGAAGGC	3245		3186	GAGATGGTGCTTATTTGGCTGCCATGCTCTGGCACAGTCCAGTGGAGCCAGGAAGGC
Db	3246	ACAGGGGTCTGA	3257		3189	GAGATGGTGCTTATTTGGCTCCCATGCTCTGGCACAGTCCAGTGGAGCCAGGAAGGC	3245		3181	GAGATGGTGCTTATTTGGCTCCCATGCTCTGGCACAGTCCAGTGGAGCCAGGAAGGC
RESULT 2	AB022696	AB022696	3610 bp	mrna	linear	PRI 31-AUG-1999				
LOCUS	DEF-NITION	AB022696	Homo sapiens mRNA for BECL1, complete cds.							
ACCESSION	VERSION	AB022696.1	G1:5804783							
KEYWORDS	SOURCE	BECL1: human BECL1	Homo sapiens (human)							
ORGANISM		Homo sapiens								
REFERENCE		Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.								
AUTHORS		1 (sites)								
TITLE		Miyake, A., Mochizuki, S., Yokoi, H., Kohda, M. and Furuichi, K.								
JOURNAL		New ether-a-go-go K(+) channel family members localized in human telencephalon								
MCLINE		J. Biol. Chem. 274 (35), 25018-25025 (1999)								
REFERENCE		2 (bases 1 to 3670)								
AUTHORS		Miyake, A., Mochizuki, S., Yokoi, H., Kohda, M. and Furuichi, K.								
TITLE		Direct Submission								
JOURNAL		Submitted (21-JAN-1999) Akira Miyake, Yamanouchi Pharmaceutical Co., Ltd., Molecular Medicine Laboratories; 21 Miyukigaoka, Tsukuba, Ibaraki 305-8585, Japan (E-mail:miyake@yamanouchi.co.jp, Tel:81-298-52-5111(ex.3324) Fax:81-298-52-5444)								

	624	a	1214	c	1114	a	658	t
BASE COUNT								
	EPV	SQ	A	E	A	T	S	I
	G	P	P	P	P	P	G	S
	G	G	L	A	L	P	N	D

Query Match	100.0%;	Score 3252;	DB 9;	Length 3610;
Best Local Similarity	100.0%;	Pred. No. 0;		

BEST LOCAL SIMILARITY 100.0%; PRED. NO. 0;
Matches 3252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGGCGGCATGCGGGGCTCTCTGGCGCTCAGAAACACCTTCTCTGACACCATCTGCTACG	60	1116	ACACTGCTCATGGCGGTGTTGCGCCTGCTCGGCACTGGGTGCGCTGCTGCTGTTTAC	1175
Db	36	ATGGCGGCATGCGGGGCTCTCTGGCGCTCAGAAACACCTTCTCTGACACCATCTGCTACG	95	1141	ATTGGCCAGCGGAGATCGAGAGCAGCAATCCGAGCTGCTGAGATTGGCTGCTGCTGCTG	1200
QY	61	CGCTTCGACGCGACACAGTAACCTTCTGCTGGCAACGCCAGGTTGGCGGCTGCTGCTG	120	1176	ATGGCCAGCGGAGATCGAGAGCAGCAATCCGAGCTGCTGAGATTGGCTGCTGCTGCTG	1235
Db	96	CGCTTCGACGCGACACAGTAACCTTCTGCTGGCAACGCCAGGTTGGCGGCTGCTGCTG	155	1201	GAGTGGCCGCCGACCTGAGAGTCCCTACTACTGCTGGTGGCCGAGGCGAGCTGAGGG	1260
QY	121	CCGCTGCTCTACTGCTGATGGGTTCGTGACCTCAGCGGCTCTCTGCGGCTGAGGTC	180	1236	GAGCTGGCCGCCGACTGGAGACTCCCTACTACTGCTGGCGGAGGCGGAGCTGGAGG	1295
Db	156	CCGCTGCTCTACTGCTGATGGGTTCGTGACCTCAGCGGCTCTCTGCGGCTGAGGTC	215	1261	AACAGCTCCGCGCAGAGTGAACCTGCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	1320
QY	181	ATGACGCGGCTGTGCT	240	1296	AACAGCTCCGCGCAGAGTGAACCTGCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	1355
Db	216	ATGACGCGGCTGTGCT	275	1321	GAGTGGTGGCGGCGCTGCTGCTGCGCAGCGCTTACATCACCTCCCTCTACTTCCGACTC	1380
QY	241	CAACAGATCCGCAAGGCCCTGGAGAGCACAAGAGTTCAAGGCTGAGCTGAGCTGATC	300	1356	GAGTGGTGGCGGCGCTGCTGCGCAGCGCTTACATCACCTCCCTCTACTTCCGACTC	1415
Db	276	CAACAGATCCGCAAGGCCCTGGAGAGCACAAGAGTTCAAGGCTGAGCTGAGCTGATC	335	1381	AGCAGCTCACACGCTGGGCTTCGCAACGCTGTCGCAACGCTGTCACACAGCAGCAGCAG	1440
QY	301	CGGAGAGCGGCTCCGCTTCTGGTGTCTCTGATGTATACCATTAAGAGATGAGAAA	360	1416	AGCAGCTCACACGCTGGGCTTCGCAACGCTGTCGCAACGCTGTCACACAGCAGCAGCAG	1475
Db	336	CGGAGAGCGGCTCCGCTTCTGGTGTCTCTGATGTATACCATTAAGAGATGAGAAA	395	1441	TTCTCATCTGCACCATCTCATCGGCGCTGATGACGCGGTGGTGGTGGTGGTGGTGG	1500
QY	361	GGGAGGTGGCT	420	1476	TTCTCATCTGCACCATCTCATCGGCGCTGATGACGCGGTGGTGGTGGTGGTGGTGG	1535
Db	396	GGGAGGTGGCT	455	1501	AGGCGCATCTCCAGCGCATGTCGCGCGCTGATGACGCGGTGGTGGTGGTGGTGGTGG	1560
QY	421	GGCCCGGACATGGAAGGACAGAGTGGTGGCGGCGCGGATATGCGGGGACGATCC	480	1536	AGGCGCATCTCCAGCGCATGTCGCGCGCTGATGACGCGGTGGTGGTGGTGGTGGTGG	1595
Db	456	GGCCCGGACATGGAAGGACAGAGTGGTGGCGGCGCGGATATGCGGGGACGATCC	515	1561	CTGGCGGACTACATCCGCTGATGCGCGCTGATGCGCGCTGATGCGCGCTGATGCGCG	1620
QY	481	AAAGGCTTCAATGCCAACCGCGGAGCGCGGCTGCTTACACCTGTCGGGAC	540	1596	CTGGCGGACTACATCCGCTGATGCGCGCTGATGCGCGCTGATGCGCGCTGATGCGCG	1655
Db	516	AAAGGCTTCAATGCCAACCGCGGAGCGCGGCTGCTTACACCTGTCGGGAC	575	1621	TTCTCCAGGCGCTGGCGGTGAAACAATGGCATCGACACCGAGCTGCTGACAGC	1680
QY	541	CTGAGAGCGGCGCAAGGACAGCTCAATTAAGGGGTGTTGGGGAGAAACCA	600	1656	TACTTCCAGGCGCTGGCGGTGAAACAATGGCATCGACACCGAGCTGCTGACAGC	1715
Db	576	CTGAGAGCGGCGCAAGGACAGCTCAATTAAGGGGTGTTGGGGAGAAACCA	635	1681	CTCCCTGACGAGCTCGCGCAGACATCGCCATGACCTGCAACAAGAGGTCTCTGACCTG	1740
QY	601	AACCTGCTGAGTACAAAGTAGCGCCATCCGGAAGTCGCCCTTCACTCTGTCACCTG	660	1716	CTCCCTGACGAGCTCGCGCAGACATCGCCATGACCTGCAACAAGAGGTCTCTGACCTG	1775
Db	636	AACCTGCTGAGTACAAAGTAGCGCCATCCGGAAGTCGCCCTTCACTCTGTCACCTG	695	1741	CCACTGTTTGGAGCGGCGCAGCGCGCTGCTGCGGCGCTGCTCTGCGGCGCTGCGGCGC	1800
QY	661	GGGCACTGAGAGCCACTGGATGGCTTCATCTGCTGCGACACTCTATGIGGCTGTC	720	1776	CCACTGTTTGGAGCGGCGCAGCGCGCTGCTGCGGCGCTGCTCTGCGGCGCTGCGGCGC	1835
Db	696	GGGCACTGAGAGCCACTGGATGGCTTCATCTGCTGCGACACTCTATGIGGCTGTC	755	1801	GCCTTCTGACGCGGCGGAGTACTCATCCACCAAGCGGATGCCCTGCGAGGCGCTCTAC	1860
QY	721	ACTGTGCTTACAGCTGTGTGAGCAGCAGCGGAGCCAGTGGCGCGCGCGCGCG	780	1836	GCCTTCTGACGCGGCGGAGTACTCATCCACCAAGCGGATGCCCTGCGAGGCGCTCTAC	1895
Db	756	ACTGTGCTTACAGCTGTGTGAGCAGCAGCGGAGCCAGTGGCGCGCGCGCGCGCG	815	1861	TTTGTCTGCTTGGCTCCATGAGGTGCTCAAGGTTGGACCGCTGCTGCGCATCTTAGGG	1920
QY	781	CCAGCGCTGTGACCTGGCGCTGAGGCTCTCTTCACTCTGACATGTGCTGAATTC	840	1896	TTTGTCTGCTTGGCTCCATGAGGTGCTCAAGGTTGGACCGCTGCTGCGCATCTTAGGG	1955
Db	816	CCAGCGCTGTGACCTGGCGCTGAGGCTCTCTTCACTCTGACATGTGCTGAATTC	875	1921	AGGCGGACTGATGGCTGTGAGTCCCGCGGCGGAGGAGTGGTAAAGGCGCATGCG	1980
QY	841	CCTACACATCTGCTCAAGTCGCGGCGAGGCTGTTTGGCCCAAGTCCNTTGGCTC	900	1956	AGGCGGACTGATGGCTGTGAGTCCCGCGGCGGAGGAGTGGTAAAGGCGCATGCG	2015
Db	876	CCTACACATCTGCTCAAGTCGCGGCGAGGCTGTTTGGCCCAAGTCCNTTGGCTC	935	1981	GACGTGAAGGGGCTGACGTACTGGCTCTGCAAGTGTCTGCAAGTGGCTGCGCTGCGAG	2040
QY	901	CACAGCTCACCACCTGGTTCCTGCTGGATGTATCGCAGCGGCTGCGCTTGTGACTGCTA	960	2016	GACGTGAAGGGGCTGACGTACTGGCTCTGCAAGTGTCTGCAAGTGGCTGCGCTGCGAG	2075
Db	936	CACAGCTCACCACCTGGTTCCTGCTGGATGTATCGCAGCGGCTGCGCTTGTGACTGCTA	995	2041	AGCCTTGGCTGTACCCCGAGTGTGCCCCCGGCTTCACTGCTGCGCTGCGCTGCGAGGG	2100
QY	961	CATGCTTCAAGGTCAAGTGTACTTTCGGGCGCCATCTGCTGAAGAGCGGCTGCTGCTG	1020	2076	AGCCTTGGCTGTACCCCGAGTGTGCCCCCGGCTTCACTGCTGCGCTGCGCTGCGAGGG	2135
Db	996	CATGCTTCAAGGTCAAGTGTACTTTCGGGCGCCATCTGCTGAAGAGCGGCTGCGCTG	1055	2101	AGCTACACCTGCTGGGTGGGAGGCTCTGACAGGTGGACACCGCTCCCTGACGGCG	2160
QY	1021	CGCTGCTCGGCTGCTTCCGCGGCTGACCGGTACTCGCAGTACAGCGGCTGCTGCTG	1080	2136	AGCTACACCTGCTGGGTGGGAGGCTCTGACAGGTGGACACCGCTCCCTGACGGCG	2195
Db	1056	CGCTGCTCGGCTGCTTCCGCGGCTGACCGGTACTCGCAGTACAGCGGCTGCTGCTG	1115	2161	GACATACCCCTTATGCTCCACGCTGGAGGAGGAGAGATGGGGAGCAGGCGCCACG	2220
QY	1081	ACATGCTCATGGCGGTGTTCCGCTGCTCGGCACTGGTCCGCTGCTGCTGCTGCTGCT	1140			

Query Match				100.0%; Score 3250.4; DB 9; Length 3853;			
Best Local Similarity				100.0%; Pred. No. 0;			
Matches 3251; Conservative 0; Mismatches 1; Indels 0; Gaps 0;							
QY	1	ATCCGCGCCATCGCGGCTCTCGCGCTCAGAACAGCTTCTCTGGACCACTGCTACG	60	DB	261	ATCCGCGCCATCGCGGCTCTCGCGCTCAGAACAGCTTCTCTGGACCACTGCTACG	320
QY	61	CGCTTCGAGCGGACGACAGTAACCTTGTGTGGCAACGCGCCAGGTGGCGGCTCTTC	120	DB	321	CGCTTCGAGCGGACGACAGTAACCTTGTGTGGCAACGCGCCAGGTGGCGGCTCTTC	380
QY	121	CCGCTGGTCTACTGTCTCATGGCTTCTGTGACCTACGCGGTCTCTCCGCGGCTGAGT	180	DB	381	CCGCTGGTCTACTGTCTCATGGCTTCTGTGACCTACGCGGTCTCTCCGCGGCTGAGT	440
QY	181	ATCGAGCGGGGTGTCGCT	240	DB	441	ATCGAGCGGGGTGTCGCT	500
QY	241	CAACAGATCGGCAAGGCTTGGACGAGCAGAGAGTCAAGGCTGAGCTGATCTGTAC	300	DB	501	CAACAGATCGGCAAGGCTTGGACGAGCAGAGAGTCAAGGCTGAGCTGATCTGTAC	560
QY	301	CGGAAGCGGGTCCCGTCTCTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	360	DB	561	CGGAAGCGGGTCCCGTCTCTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	620
QY	361	GGGAGGTGGCT	420	DB	621	GGGAGGTGGCT	680
QY	421	GGCCCGCAGAGTGAAGGAGACAGGTGTGGCGGCGCGATATGGCGGCGCAGATCC	480	DB	681	GGCCCGCAGAGTGAAGGAGACAGGTGTGGCGGCGCGATATGGCGGCGCAGATCC	740
QY	481	AAAGGCTTCATGCCAACCGGCGGAGCGGCGGCTCTCTCTCTCTCTCTCTCTCTCT	540	DB	741	AAAGGCTTCATGCCAACCGGCGGAGCGGCGGCTCTCTCTCTCTCTCTCTCTCTCT	800
QY	541	CTCAGAACGAGCCCAAGGCAAGCAGCAAGCTCAATAGGGGCTGTTGGGGAAGACCA	600	DB	801	CTCAGAACGAGCCCAAGGCAAGCAGCAAGCTCAATAGGGGCTGTTGGGGAAGACCA	860
QY	601	AACCTGCCTGAGTACAAAGTACCGCCATTCGGAAGTGGCCCTTCATCCTGTGCACTG	660	DB	861	AACCTGCCTGAGTACAAAGTACCGCCATTCGGAAGTGGCCCTTCATCCTGTGCACTG	920
QY	661	GGGGCACTGAGAGCCACCTGGATGGCTTCATCTGCTCGCCACACCTGATGTGCTGTC	720	DB	921	GGGGCACTGAGAGCCACCTGGATGGCTTCATCTGCTCGCCACACCTGATGTGCTGTC	980
QY	721	ACTGTCCCTTACAGCTGTGTGTGAGCAGCAGCAGGAGCCAGTCCCGCCGCGCCGCG	780	DB	981	ACTGTCCCTTACAGCTGTGTGTGAGCAGCAGCAGGAGCCAGTCCCGCCGCGCCGCG	1040
QY	781	CCAGGCTGTGAGCTGGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	840	DB	1041	CCAGGCTGTGAGCTGGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	900
QY	841	CGTACCACATTCGCTGCCAAGTGGGCGCAGGTGGTGTTCGCCCAAGTCCATTTGCCCT	900	DB	1101	CGTACCACATTCGCTGCCAAGTGGGCGCAGGTGGTGTTCGCCCAAGTCCATTTGCCCT	1160
QY	901	CATAGCTCACACCTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	960	DB	1161	CATAGCTCACACCTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1220
QY	961	CATGCGCTTCAAGTCAACGTGTACTTCGGGGCCCATCTCTCTGAAGACGCTGGCGCTG	1020	DB	1221	CATGCGCTTCAAGTCAACGTGTACTTCGGGGCCCATCTCTCTGAAGACGCTGGCGCTG	1080
QY	1021	CGCCTGCTCGGCTGCTCCGGGCTGGACCGGTACTCGCAGTACAGCGCGCTGGTCTG	1080	DB	1281	CGCCTGCTCGGCTGCTCCGGGCTGGACCGGTACTCGCAGTACAGCGCGCTGGTCTG	1140
QY	1081	ACACTCTCTATGGCGGTGTTCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1140	DB	1341	ACACTCTCTATGGCGGTGTTCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1200
QY	1141	ATTGGCCAGCGGAGATCGAGAGCAGGAATCCGAGCTGCTGAGATTTGGCTGCTGAG	1200	DB	1401	ATTGGCCAGCGGAGATCGAGAGCAGGAATCCGAGCTGCTGAGATTTGGCTGCTGAG	1260
QY	1201	GAGCTGGCGCGGCTGAGAGTCTCTACTACTCTGTTGGCGCGGAGGCCAGCTGGAGG	1260	DB	1461	GAGCTGGCGCGGCTGAGAGTCTCTACTACTCTGTTGGCGCGGAGGCCAGCTGGAGG	1320
QY	1261	AACAGCTCGGCGCAGAGTACAACTGACAGCAGCAGCAGGAGCCAGGGAGCGGCTG	1320	DB	1521	AACAGCTCGGCGCAGAGTACAACTGACAGCAGCAGCAGGAGCCAGGGAGCGGCTG	1380
QY	1321	GAGCTGCTGGCGGCGGCTGCTGGCGAGGCTTACATCTCTCTCTCTCTCTCTCTCTCT	1380	DB	1581	GAGCTGCTGGCGGCGGCTGCTGGCGAGGCTTACATCTCTCTCTCTCTCTCTCTCTCT	1440
QY	1381	AGCAGCTCACCAGGCTGGGCTTCGCGCAACGCTGTCCGCAACAGCGACACCGCAAGATC	1440	DB	1641	AGCAGCTCACCAGGCTGGGCTTCGCGCAACGCTGTCCGCAACAGCGACACCGCAAGATC	1500
QY	1441	TTCTCCTCTGACCATGCTCATCGGCGCCTGTATGACGCGGTGGTGTGTTGGGAAGCTG	1500	DB	1701	TTCTCCTCTGACCATGCTCATCGGCGCCTGTATGACGCGGTGGTGTGTTGGGAAGCTG	1560
QY	1501	ACGGGCTCATCGAGGCTGTACGCGCGGCTTCTGTACACAGCGCGCAGCGGCGAC	1560	DB	1761	ACGGGCTCATCGAGGCTGTACGCGCGGCTTCTGTGTACACAGCGCGCAGCGGCGAC	1620
QY	1561	CTCGGCTATCATCGGCTATCCCGGTATCCCGAGGCTTCAAGAGCGGCTGCTGAGG	1620	DB	1821	CTCGGCTATCATCGGCTATCCCGGTATCCCGAGGCTTCAAGAGCGGCTGCTGAGG	1680
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QY	1681	CTCCCTGACAGCTGCGCGCAGACATTCGCTATGACCTGCAACAGGAGTCTGAGGCTG	1740	DB	1941	CTCCCTGACAGCTGCGCGCAGACATTCGCTATGACCTGCAACAGGAGTCTGAGGCTG	1800
QY	1741	CCACTGTTGAGCGGCGCAGCGGCTGCTGCGGCGCTCTCTCTGCGGCTGCTGAGG	1800	DB	2001	CCACTGTTGAGCGGCGCAGCGGCTGCTGCGGCGCTCTCTCTGCGGCTGCTGAGG	1860
QY	1801	GCCTTCTGACCGCGCGGCTGACCTTATCCACAGGCTGATGCGCTGAGGCTGCTGAGG	1860	DB	2061	GCCTTCTGACCGCGCGGCTGACCTTATCCACAGGCTGATGCGCTGAGGCTGCTGAGG	1920
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QY	1981	GAGCTGAAGGGCTGACGTACTGCTGCTGAGTGTCTGACGCTGGCTGGCTGCTGAGG	2040	DB	2241	GAGCTGAAGGGCTGACGTACTGCTGCTGAGTGTCTGACGCTGGCTGGCTGCTGAGG	2100
QY	2041	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	2100	DB	2301	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	2160
QY	2101	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	2160	DB	2361	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	2220
QY	2161	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	2220	DB	2421	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	2280
QY	2221	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	2280	DB	2481	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	2340
QY	2281	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	2340	DB	2541	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	2400
QY	2341	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	2400	DB	2601	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	2460
QY	2401	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	2460	DB	2661	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	2520
QY	2461	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	2520	DB	2721	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	2580
QY	2521	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	2580	DB	2781	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	2640
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QY	2641	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	2700	DB	2901	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	2760
QY	2701	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	2760	DB	2961	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	2820
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QY	2941	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	3000	DB	3201	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	3060
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QY	3181	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	3240	DB	3441	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	3300
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QY	3301	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	3360	DB	3561	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	3420
QY	3361	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	3420	DB	3621	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	3480
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QY	3661	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	3720	DB	3921	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	3780
QY	3721	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	3780	DB	3981	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	3840
QY	3781	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	3840	DB	4041	AGCTTCCGCTGTACCGCGGCTTGCCTGCGCTTCACTGCTGGCTTCCGAGGAGGCTC	3900
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REFERENCE 1 (bases 1 to 3249)			
AUTHORS Jegla, T. and Wickender, A.			
TITLE Human elk a voltage-gated potassium channel subunit			
JOURNAL Patent: US 6413741-A 2 02-JUL-2002;			
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ORIGIN			
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Best Local Similarity 99.9%; Pred. No. 0;			
Matches 3247; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
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Qy	121	CCGCTGCTCTACTGCTCTGATGCTTCTGTGACCTCAGGGCTTCTCCCGGCTGAGTC	180
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Qy	181	ATGACGCGGGCTTGCCCTGCTCTTATGGCCAGACACAGTGAAGTGAAGTGAAGTGA	240
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Qy	301	CGGAAGAGCGGCTCCCGTTCTGCTGCTCTGATGATGATGATGATGATGATGATGAT	360
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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A potassium channel member of the erq family
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LOCUS AR212361 3857 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 19 from patent US 6399761.
ACCESSION AR212361
VERSION AR212361.1 GI:21515915
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 3857)
AUTHORS Miller, A.P., Hu, P., Curran, M. Edward., Rutter, M. and Jiang-Yang, W.
TITLE Nucleic acid encoding human potassium channel K+ nov1 protein
JOURNAL Patent: US 6399761-A 19-04-JUN-2002;
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Q	y	3181	GAGATGGTGCTATTGGCTGCATGGCTCTGGCACAGTCCAGTGGACCCAGGAGAGAGGC	3240
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LOCUS AR281263				
DEFINITION Sequence 1 from patent US 6518398.				
ACCESSION AR281263				
VERSION AR281263.1 GI:29716863				
KEYWORDS Unknown.				
SOURCE Unknown.				
ORGANISM Unclassified.				
REFERENCE 1 (bases 1 to 3355)				
AUTHORS Curtis,R.A.J.				
TITLE ERG potassium channel				
JOURNAL Patent: US 6518398-A 1 11-FEB-2003;				
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BASE COUNT 580 a 1128 c 1041 g 606 t				
ORIGIN				
Query Match 97.0%; Score 3156; DB 6; Length 3355;				
Best Local Similarity 98.2%; Pred. No. 0;				
Matches 3192; Conservative 0; Mismatches 60; Indels 0; Gaps 0;				
Q	y	1	ATGCGGGCATGGGGGCTCTCGGGCGCTCAGAACACCTTCTCGNACCATCGCTACG	60
D	b	104	ATGCGGGCATGGGGGCTCTCGGGCGCGCAGAACAACCTTCTCGNACCATCGCTACG	163
Q	y	61	CGCTTCAGCGGCACGACAGTAACCTTCGTCTGGGCAACGCCAGGTGGGGGCTCTTC	120
D	b	164	CGCTTCAGCGGCACGACAGTAACCTTCGTCTGGGCAACGCCAGGTGGGGGCTCTTC	223
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RESULT: 7
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KEYWORDS
SOURCE      .
ORGANISM    . Unknown.
REFERENCE   . Unknown.
AUTHORS     . Unclassified.
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TITLE       Curtis,R.A.J.
JOURNAL     ERG potassium channel
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ORIGIN
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BB      104 ATGCGGGCCATGCGGGGCGCTCTGGCGGCGGAGAACACCTTCTCTGGACACCATCGCTACG 163
QY      61  CGCTTCAGCGGCACGCACAGTAACCTTCGTCTGGCCAAACCCAGGTGGCGGGGCTCTTC 120
DB      164 CGCTTCAGCGGCACGCACAGTAACCTTCGTCTGGCCAAACCCAGGTGGCGGGGCTCTTC 223
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Db 224 CCCGTGGTCTACGTCTCTGATGGCTCTGTGACCTCAGGGCTCTCTCCCGGGCTGAGGTC 243
Qy 181 ATGCAGCGGGCTGTGCTGTCTCTCTCTATGCGCCACACACAGAGAGCTGTGCTCGC 240
Db 284 ATGCAGCGGGCTGTGCTGTCTCTCTCTATGCGCCACACACAGAGAGCTGTGCTCGC 343
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Db 1664 CTGCGCGACTACATCCGCGCATCCAGCTATCCCAAGCCCTTCAAGCAGCGCATGCTGGAG 1723
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Db 1784 CTCCCTGACGAGCTGCGCGCAGACATCGCCATGCACCTGCAACAGAGAGTCTGCGAGCTG 1843
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Db 1904 GCCTTCTCAGCGCGGGGAGTACTCTATCCACCAAGCGATGCCCTGCAAGGCCCTCTAC 1963
Qy 1861 TTGTGCTGCTGCGCTCCATGGAGTGTCTAAGGTTGCGACCGTGTCTGCCATGCTAC 1920
Db 1964 TTGTGCTGCTGCGCTCCATGGAGTGTCTAAGGTTGCGACCGTGTCTGCCATGCTAC 2023
Qy 1921 AAGGGACCTCATCGCTGTGCTGCGCGCGGAGAGTGTGTTAAAGCCACGCGC 1980
Db 2024 AAGGGTACCTCATCGCTGTGAGCTGCCCGGAGGAGAGTGTGTTAAAGCCACGCGC 2083
Qy 1981 GAGGTAAAGGGCTGACGTACTGCGTCTGCAAGTGTCTGCAAGTGGGTGGCTGCACTAC 2040
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Db 2324 GTCCTCCAGCGCCAGCTGATGAGCCCTCAGCCCTGCTGTGCTGCTGCTGCTGCTC 2383
Qy 2281 TCATCCTCAGCTGCGCAAGCTGTATCCCGACGTCGAACAGCAGCCCGGCTGCTGCTAGGT 2340
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QY	2341	GGCAGAGGAGGCCAGGCGAGGCGCTTTGAAGGCTGAGGCTGGCCCTCTGCTCC	2400	ORGANISM	Unknown.	
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QY	2401	CCACGGCCCTAGAGGGCTACGGCTGCCGCCATGCCATGGATGTGCCCCAGATCTG	2460	AUTHORS	1 (bases 1 to 3249);	
Db	2504	CCACGGCCCTAGAGGGCTACGGCTGCCGCCATGCCATGGATGTGCCCCAGATCTG	2563	TITLE	Curtis R.A.J.	
QY	2461	AGCCCAAGGTATGATGGCATTAAGACGGCTGTGGCTGGACCCAGCCAAATTTCT	2520	JOURNAL	ERG potassium channel	
Db	2564	AGCCCAAGGTATGATGGCATTAAGACGGCTGTGGCTGGACCCAGCCAAATTTCT	2623	PATENT	US 6518398-A 3 11-FEB-2003;	
QY	2521	TTCCGGCTGGCCAGCTTGGCCCGAATGTAGACAGCAGCCCTCCCTGGACCAAGC	2580	LOCATION/QUALIFIERS	Location/Qualifiers	
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QY	2581	GBCCTGCTCACTGTTCCCAATGGGCCAGGCAAGGAACACAGACACTGGACAG	2640	BASE COUNT	570 a 1089 c 600 t	
Db	2684	GBCCTGCTCACTGTCCCAATGGGCCAGGCAAGGAACACAGACACTGGACAG	2743	ORIGIN		
QY	2641	CTTCGGCAGGCGGTACAGAGCTGTACAGCAGGTGTGTCAGATGGCGGAGAGCTCAG	2700	Query Match	97.0%; Score 3153; DB 6; Length 3249;	
Db	2744	CTTCGGCAGGCGGTGTAGAGCTGTACAGCAGGTGTGTCAGATGGCGGAGAGCTCAG	2803	Best Local Similarity	98.2%; Pred. No. 0;	
QY	2701	TCACCTTCGCGAGGCTGTGAGCTTGTGTCGCGCCACAGGAGGTTGCTGCGCTCGG	2760	Matches 3189; Conservative	0; Mismatches 60; Indels 0; Gaps 0;	
Db	2804	TCACCTTCGCGAGGCTGTGAGCTTGTGTCGCGCCACAGGAGGTTGCTGCGCTCGG	2863	1	ATGCCGCGCATCGGGGCTCTCTGGCCCTCAGAACACCTTCTCTGGACACCACTGCGTAGC	
QY	2761	GCATCGGAGAGGGCGGTGCCACGACAGCTTCCGGGCTTCTGACAGCTCTGTGTG	2820	Db	1	ATGCCGCGCATCGGGGCTCTCTGGCCCTCAGAACACCTTCTCTGGACACCACTGCGTAGC
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QY	2881	TGGCCCAACCTCTGCGGGGCTCTCTCCCTCATGGCACCTCGGCTGGGCTGCCCA	2940	Db	241	CAACAGATCCCAAGAGGCTTGGACGACCAAGAGTTCAAGGCTGAGCTGTATCTGTAC
Db	2984	TGGCCCAACCTCTGCGGGGCTCTCTCCCTCATGGCACCTCGGCTGGGCTGCCCA	3043	QY	301	CGGAAGAGCGGCTCCCGTCTGTGTCTCTCTGGATGTATACCATTAAGCAATGAGAAA
QY	2941	GGCTCTCAGAGCTCCCTTGGCTCGAGCCACAGCTTCTGGAGCTCCACCTCAGACTCA	3000	Db	301	CGGAAGAGCGGCTCCCGTCTGTGTCTCTCTGGATGTATACCATTAAGCAATGAGAAA
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QY	3121	ACTGGAGACCCCGACAGGCTAGGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG	3180	Db	481	AAAGGCTTCAATGCCAACCGCGGAGCGGCGCTGTCTTACCACTGTCTCGGCGAC
Db	3224	ACTGGAGACCCCGACAGCTGTCAGGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG	3283	QY	541	CTGCAGAGCAGCCCAAGGCAAGCACAAGCTCAATTAAGGGGTGTGTGGGAGAAACCA
QY	3181	GAGATGGCTTATTGGCTGCCATGGCTGTGGCAGAGTCCAGTGGACCCAGGAAGAGGC	3240	Db	541	CTGCAGAGCAGCCCAAGGCAAGCACAAGCTCAATTAAGGGGTGTGTGGGAGAAACCA
Db	3284	GAGATGGCTTATTGGCTGCCATGGCTGTGGCAGAGTCCAGTGGACCCAGGAAGAGGC	3343	QY	601	AACTTGCCTGAGTCAAAAGTAGCCCATCGGAAGTGCCTTCTCTGTGCACTGT
QY	3241	ACAGGGGTCTGA 3252		Db	601	AACTTGCCTGAGTCAAAAGTAGCCCATCGGAAGTGCCTTCTCTGTGCACTGT
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RESULT 8				Db	661	GGGCACTGAGAGCAGCTTGGATGGCTTATCTGCTCGCCACACTCTATGTGGGTGT
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DEFINITION	Sequence 3 from patent US 6518398.			Db	721	ACTGTGCCCTACAGGCTGTGTGTCAGACAGCAGGAGCGGCGGCTGTCTTACCACTGTCTCGGCGAC
ACCESSION	AR281264			QY	781	CCACAGCTGTGTGACCTGGCGGTGGAGGTGCTCTTCTTCACTCTGACACTGTGTGTAATTC
VERSION	AR281264.1	GI:29716864		Db	781	CCACAGCTGTGTGACCTGGCGGTGGAGGTGCTCTTCTTCACTCTGACACTGTGTGTAATTC
KEYWORDS	Unknown.			QY	841	CGTACCACTTCTGTGTCCCAAGTGGGCGGAGGTGGTGTGTTCGCCCAAGTCCATTTGCCCTC
SOURCE				Db	841	CGTACCACTTCTGTGTCCCAAGTGGGCGGAGGTGGTGTGTTCGCCCAAGTCCATTTGCCCTC

Db	841	CGTACCACATTCGTGTCACAAATCGGSCCAAGTGTGTCTTGGCCCAAGTCCATTTCCTC	900
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Db	901	CATTAGTACACACCTGGTTCCTGCTGSAITGTCATCGAGCGCTGCCCTTTGACCTGCTG	960
Qy	961	CATGCTTCAAGTCAACCTGTACTTCGGGGGCCAATCTGCTCAAGACGGTGGCTGCTG	1020
Db	961	CATGCTTCAAGTCAACCTGTACTTCGGGGGCCAATCTGCTCAAGACGGTGGCTGCTG	1020
Qy	1021	CGCTGCTGGCTGCTGCTCCGGGCTGACCCGGTACTCGAGTACAGCGCGTGGTCTG	1080
Db	1021	CGCTGCTGGCTGCTGCTCCGGGCTGACCCGGTACTCGAGTACAGCGCGTGGTCTG	1080
Qy	1081	ACACTGCTATGCGCTGTTCGCCCTGCTCGCGCACTGGTGGCTGCTGCTGCTGCTTAC	1140
Db	1081	ACACTGCTATGCGCTGTTCGCCCTGCTCGCGCACTGGTGGCTGCTGCTGCTGCTTAC	1140
Qy	1141	ATTGGCCAGCGGAGATCGAGACAGCGAATCCGAGTCCCTGAGATGGCTGCTGCTG	1200
Db	1141	ATTGGTCAGCGGAGATCGAGACAGCGAATCCGAGTCCCTGAGATGGCTGCTGCTG	1200
Qy	1201	GAGTGGCCCGGCTGCTGAGACTCCCTACTACCTGGTGGCGGAGCCAGCTGAGGG	1260
Db	1201	GAGTGGCCCGGCTGCTGAGACTCCCTACTACCTGGTGGCGGAGCCAGCTGAGGG	1260
Qy	1261	AACAGTCCGGCAGAGTGAACCTGACAGCAGCAGCAGCGAGCGGACCGGGCTG	1320
Db	1261	AACAGTCTGGCCAGAGTGAACCTGACAGCAGCAGCAGCGAGCGGACCGGGCTG	1320
Qy	1321	GAGTGTGGGGGGCCGCTGCTGCGCAGCGCTACATCACTCCCTCTACTTCGCACTC	1380
Db	1321	GAGTGTGGGGGGCCGCTGCTGCGCAGCGCTACATCACTCCCTCTACTTCGCACTC	1380
Qy	1381	AGCAGCTTACAGCTGGGCTTGGCAACAGTGTCCGCCACACAGCGACCCGAGAGATC	1440
Db	1381	AGCAGCTTACAGCTGGGCTTGGCAACAGTGTCCGCCACACAGCGACCCGAGAGATC	1440
Qy	1441	TTCTCCATGTGACCATGCTCATCGCGCCCTGATGACAGCGGCTGTGTGGGAAGCTG	1500
Db	1441	TTCTCCATGTGACCATGCTCATCGCGCCCTGATGACAGCGGCTGTGTGGGAAGCTG	1500
Qy	1501	ACGGCATATCCAGCGCATGTACGCCCGCGCTTCTCTATCCACAGCCGACCGCGAC	1560
Db	1501	ACGGCATATCCAGCGCATGTACGCCCGCGCTTCTCTATCCACAGCGCGCGCGAC	1560
Qy	1561	CTCGGGAGTACATCCGATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG	1620
Db	1561	CTCGGGAGTACATCCGATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG	1620
Qy	1621	TACTTCAGCCCACTGGCGGTGAACATGGCATGCGACACCGAGCTGCTCGAGAGC	1680
Db	1621	TACTTCAGCCCACTGGCGGTGAACATGGCATGCGACACCGAGCTGCTCGAGAGC	1680
Qy	1681	CTCCCTGAGAGTGGCGCAGACATCGCCATGCACTGCAACAGGAGTCTCTGCACTG	1740
Db	1681	CTCCCTGAGAGTGGCGCAGACATCGCCATGCACTGCAACAGGAGTCTCTGCACTG	1740
Qy	1741	CCACTGTTGAGCGCCAGCCGCGGCTGCTTGGGGCACTGTCTGTGGCCCTGCGGCC	1800
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Qy	1801	GCCTTCTGACGCGCGGCGAGTACCTCATCCACAAAGCGGATGCCCTGACGGCCCTAC	1860
Db	1801	GCCTTCTGACGCGCGGCGAGTACCTCATCCACAAAGCGGATGCCCTGACGGCCCTAC	1860
Qy	1861	TTTGTCTGTCTGGCTTCCATGAGAGTGTCAAGGTGCAACCGTGTCTGCACTAGGG	1920
Db	1861	TTTGTCTGTCTGGCTTCCATGAGAGTGTCAAGGTGCAACCGTGTCTGCACTAGGG	1920
Qy	1921	AAGGGCACTGATGGCTGTGAGCTGCCCGGGGAGAGAGTGTAAAGGCCATGCC	1980
Db	1921	AAGGGCACTGATGGCTGTGAGCTGCCCGGGGAGAGAGTGTAAAGGCCATGCC	1980

Db	1921	AAGGCTGACCTGATGGCTGTGAGCTGCCCGGGGAGAGAGTGTAAAGGCCATGCC	1980
Qy	1981	GACGTAAAGGGCTGACGTACTGGTCTCTGAGTGTCTGAGCTGGCTGGCTGGACAC	2040
Db	1981	GACGTAAAGGGCTGACGTACTGGTCTCTGAGTGTCTGAGCTGGCTGGACAC	2040
Qy	2041	AGCCTTGGCTGTACCCCGAGTTTGGCCCGGCTTACGCCGTGGCTTCCGAGGGAGCTC	2100
Db	2041	AGCCTTGGCTGTACCCCGAGTTTGGCCCGGCTTACGCCGTGGCTTCCGAGGGAGCTC	2100
Qy	2101	AGCTAACACCTGGTGTGGGGAGGCTTCTGAGAGAGTGGACACAGCTTCCCTGAGCGGC	2160
Db	2101	AGCTAACACCTGGTGTGGGGAGGCTTCTGAGAGAGTGGACACAGCTTCCCTGAGCGGC	2160
Qy	2161	GACATACCTCTATGTCCAGCTGAGAGAGAGACAGATGGAGAGAGCGCCGAC	2220
Db	2161	GACATACCTCTATGTCCAGCTGAGAGAGAGAGACAGATGGAGAGAGCGCCGAC	2220
Qy	2221	GTCTCCCGAGCCAGCTGATGAGCCCTCCAGCCCTGCTGTCTGCTGCTGCTGCTGCT	2280
Db	2221	GTCTCCCGAGCCAGCTGATGAGCCCTCCAGCCCTGCTGTCTGCTGCTGCTGCTGCT	2280
Qy	2281	TCATCTCAGCTGCCAGCTGCTATCCAGCTGCTGACAGACACCGCGCTGCTGCTGCT	2340
Db	2281	TCATCTCAGCTGCCAGCTGCTATCCAGCTGCTGACAGACACCGCGCTGCTGCTGCT	2340
Qy	2341	GGCAGAGGAGCGCAGCGCAGGGCTTTGAAGGCTGAGCTGGCTGGCTGGCTGGCTGG	2400
Db	2341	GGCAGAGGAGCGCAGCGCAGGGCTTTGAAGGCTGAGCTGGCTGGCTGGCTGGCTGG	2400
Qy	2401	CCAGCGGCTTAGAGGGCTGACGCTGCGCCCATGCTGCTGCTGCTGCTGCTGCTGCT	2460
Db	2401	CCAGCGGCTTAGAGGGCTGACGCTGCGCCCATGCTGCTGCTGCTGCTGCTGCTGCT	2460
Qy	2461	AGCCCGAGGCTAGTAGAGTGGATTTGAAGGCTGAGCTGGCTGGCTGGCTGGCTGG	2520
Db	2461	AGCCCGAGGCTAGTAGAGTGGATTTGAAGGCTGAGCTGGCTGGCTGGCTGGCTGG	2520
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DB 3121 ACTGAGAGGCCCCACACAGGTGAGGGGGCTGGCCCTGAGGACCCACAGAGCTG 3180
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QY 3241 ACAGGGGTC 3249
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RESULT 9
RNO7627 Rattus norvegicus mRNA for ELK channel 2. linear RCD 05-OCT-1998
LOCUS RNO7627
DEFINITION Rattus norvegicus mRNA for ELK channel 2.
ACCESSION AJ007627
VERSION 1
KEYWORDS elk2 gene; potassium channel.
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathu.; Muridae; Murinae;
Rattus.
1
Engeland,B., Neu,A., Ludwig,J., Koepfer,J. and Pongs,O.
Identification of three rat potassium channel genes homologous to
D. melanogaster elk
Unpublished
2 (bases 1 to 3595)
Engeland,B.
Direct Submission
Submitted (03-JUL-1998) Engeland B., Zentrum fuer Molekulare
Neurobiologie Hamburg, Institut fuer Neura.le Signalverarbeitung,
Martinistrasse, D-20246 Hamburg, GERMANY
FEATURES
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[illegible]

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Best Local Similarity	89.0% Pred No. 0;				
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Qy	1732	CTGAGAGCTTCTCCGAGTGGCGGCGAGCTTCCGCGCTTCCGCGCTTCCGCGCT	1791		

Db	1896																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
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Df	544	GCCACCTTGGCCCGCGGCGGAGGAGGATGAAGCCCAATATGAAGTGTGTGAGCCA	603
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Df	604	AAGCCATAGTGCAGGAGTACAAAGTGGCTCCGTGGGGGGTCTGCTGCCCTCCCTC	663
Qy	655	CACGTGGGCACTGAGAGCCACTGGATGGCTTCACTCTGCTGCGCACACTATG-TG	714
Df	664	CACACAGCTTCCAAAGGCACTGGGAGGGCTTATCCTCTGCCACCTTCTACGTT	723
Qy	715	GCTGTCACTGTGCCCTACAGCGTGTGTGAGCACAGCAGGAGGCCAGTGGCGGCGC	774
Df	724	CGGTCCAGCTCCCTACAAATGTCTGTTCTCGGTAAGCATGACAGCCCACTACTCG	783
Qy	775	GGCGCGCCAGCTGTGACCTGGCGGTGGAGTCTCTTCTATCTGCTGCGCACACTATG	834
Df	784	CGACACACCTTGTACAGCAGATCGCGGTGAATGCTTTCATCTAGATATCATCTCG	843
Qy	835	AATTTCGTACACATCTGTTCCAAAGTCGGCGAGTGGTGTTCGCCCAAGTCCAT	894
Df	844	AACATCCGACCACTATGTCTCCAGTCCGCGCAGGTAATCTCTGCTCTCTCTCAAT	903
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Df	904	GGCTCCACTACCTGGCCACTGGTCTTCATGACCTTATGCTCTGTCCTGCTTGAC	963
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Df	1144	TATGTATCGGCGCGGAGATGAGGCCAATGACCGGTGCTCTGGGACATTTGGCTGG	1203
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Df	1480	AAGACCTCAAGGACTTCACTCGGTGTGACCGCTGCGCGCGCGTCAAGCAGCGCATG	1539
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Df	1540	CTCGAATATCTCCAGACCACTGGCGCTCAACAGCGCATCGACCGCAACGATGATG	1599
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VERSION	AB022698.1	GI:5804787	
KEYWORDS	BEC2; human BEC2.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (sites)		
AUTHORS	Miyake, A., Mochizuki, S., Yokoi, H., Kohda, M. and Furuichi, K.		
TITLE	New ether-a-go-go K(+) channel family members localized in human telencephalon		
JOURNAL	J. Biol. Chem. 274 (35), 25018-25025 (1999)		
MEDLINE	99386988		
PUBMED	10455180		
REFERENCE	2 (bases 1 to 3920)		
AUTHORS	Miyake, A., Mochizuki, S., Yokoi, H., Kohda, M. and Furuichi, K.		
TITLE	Direct Submission		
JOURNAL	Submitted (21-JAN-1999) Akira Miyake, Yamanouchi Pharmaceutical Co., Ltd., Molecular Medicine Laboratories; 21 Miyukigaoka, Tsukuba, Ibaraki 305-8585, Japan (E-mail: miyake@yamanouchi.co.jp. Tel: 81-298-52-5111 (ex. 3324), Fax: 81-298-52-5444)		
FEATURES	Location/Qualifiers		
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ORIGIN		
Query Match 27.2% Score 884.8; DB 9; Length 3920;		
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DB	574	CAGCGTCTGCACAAGGCCCTGGAGGCGCACCAGAGCAGCGGCTGAAATCTCTCTAC 633
QY	301	CGGAAGAGGGGCTCCGCTCTGTGTCTCTGTATGTATACCCATCAAGATATGAAGA 360
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QY	535	GGGCACTTCGAGAAGCAGCCCAAGGCAAGCACAAGCTCAATAAGGGGGTGTTCGGGAG 594
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QY	1495	AAGTGAAGGCTCATCATCAGGCGATGACGCGCGGCTTCTGTGTACCAAGCGGAGCG 1554
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QY	1555	CGGAGCTGCGGCTCATCTCGCATCCAGCTATCCCAAGCGGCTCAAGCAGCGGATG 1614
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QY	1615	CTGGAGTACTTCAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1674
DB	1870	CTGCAATCTTCAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1929

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2003, 15:33:19 : Search time 798 Seconds
(without alignments)
11000.717 Million cell updates/sec

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Perfect score: 3252
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs. 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3252	100.0	3323	20	AAx84910 Human brain specif
2	3250.4	100.0	3829	21	AA287712 Human ESK1 (hESK1)
3	3245.8	99.8	3249	21	AA250119 Human Elk voltage
4	3244	99.8	3252	21	AA414893 DNA encoding a her
5	3218	99.0	3857	20	AA211906 Human potassium ch
6	3156	97.0	3355	21	AA250452 Monkey potassium c
7	2664.8	81.9	3715	20	AAx84919 Rat brain specific
8	884.8	27.2	3064	20	AAx84911 Human brain specif

9	869.8	26.7	3736	20	AAx84918 Rat brain specific
10	844.4	26.0	1132	21	AA250454 Human potassium ch
11	794.4	24.4	3742	21	AA293334 Rat elk1 potassium
12	761.2	23.4	5107	21	AA250455 Human potassium ch
13	601	18.5	10579	22	ABA20014 Human nervous syst
14	601	18.5	10579	22	AAK70045 Human immune/haema
15	601	18.5	28995	22	ABA20015 Human nervous syst
16	601	18.5	28995	22	AAK70046 Human immune/haema
17	601	18.5	28995	22	AAK79967 Human immune/haema
18	601	18.5	28995	22	AAK85213 Human immune/haema
19	572.4	17.6	2694	21	AA250453 Human potassium ch
20	561.2	17.3	20974	23	AA250453 DNA encoding novel
21	384	11.8	464	21	AA293335 Rat elk2 potassium
22	365.6	11.2	3164	22	AB258129 Human potassium ch
23	364.2	11.2	4112	23	ABL08835 Drosophila melanog
24	364	11.2	3135	25	ABX12009 Transporters and i
25	362.4	11.1	2746	24	ABK88234 Human erg2 (h-erg2
26	362.4	11.1	2877	24	AA44675 Human transporter
27	362.4	11.1	2983	24	ABK88231 cDNA sequence enco
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37	338.6	10.4	1780	25	ABV75862 Human potassium ch
38	317.2	9.8	426	22	AAI98635 Human excretory re
39	317.2	9.8	426	22	AAI63031 Human kidney relat
40	303	9.3	2886	21	AA235716 Human potassium io
41	303	9.3	3002	21	AA235721 Human eag related
42	296	9.1	2746	25	ABX12013 Transporters and i
43	296	9.1	2779	22	AAI27279 Human transporter
44	290.8	8.9	350	22	ABA14086 Human nervous syst
45	281.2	8.6	2967	21	AA235717 Human potassium io

ALIGNMENTS

RESULT 1

AAx84910

ID AAx84910 standard; DNA; 3323 bp.

XX

AC AAx84910;

XX

DT 28-SEP-1999 (first entry)

XX

DE Human brain specific potassium channel protein coding sequence.

XX

FW Brain specific potassium channel; human; central nervous system disorder;

XX

KW dementia; cerebral ischaemic sclerosis; therapy; ss.

XX

OS Homo sapiens.

XX

FH Key

XX

CDS 6..3257

XX

FT /*tag= a

XX

PN WO9937577-A1.

XX

PD 29-JUL-1999.

XX

PF 20-JAN-1999; 99WO-JP00190.

XX

PR 04-DEC-1998; 98JP-0346198.

XX

PR 23-JAN-1998; 98JP-0011434.

XX

PA (YAMA) YAMANOUCHI PHARM CO LTD.

XX

MI Miyake A, Mochizuki S, Yokoi H;

Ds	1866	ITGTCTGCTCTGCTCCATGAGGCTGCTCAAGGCTGGCACCGTCTCTGGCATCTAGGG	1925
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Ds	1986	GAGTGAAGGGGTGACGTACTGCGTCTGCTGAGTGTCTGACAGTGGCTGCGCTGACAG	2045
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Ds	2046	AGCTTTGCGCTGTACCCAGTTTGGCCGGGCTTCAGTCTGTGCGCTCCGAGGGAGCTC	2105
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Ds	2106	AGCTACAACCTGGTCTGGGGAGGCTCTCCAGAGTGGACACAGTCTCCCTGAGCGGC	2165
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Ds	2166	GACAATACCTTTATGTCCACGCTGGAGGAGGAGACAGATGGGGAGGAGGCCGCCACG	2225
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Ds	2226	GTCTCCCGACCCAGCTGATGAGCCCTCCAGCCCTGCTGCTCCCTGGCTGGCACCTCC	2285
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Qy	2461	AGCCGAGGCTAGTACATGGCATTTGAAGAGGCTGAGGCTGGCCCTCTGTCTCT	2520
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Ds	2526	TTCCGGGTGGCCAGTCTGGCCCGAATGTACAGACGCGCTCCCTCGGACGAGAGC	2585
Qy	2581	GGCTGCTACTGTTCCCATGGCCAGCGAGGCAAGCAACAGACACACTGGACAAG	2640
Ds	2586	GGCTGCTACTGTTCCCATGGCCAGCGAGGCAAGCAACAGACACACTGGACAAG	2645
Qy	2641	CTTCGGCAGCGGTGACAGCTGTGACAGCAGGCTGCTGACAGTCCGGAAGGACTGCAG	2700
Ds	2646	CTTCGGCAGCGGTGACAGCTGTGACAGCAGGCTGCTGACAGTCCGGAAGGACTGCAG	2705
Qy	2701	TCATCTGCGCAGCTGTGAGCTTTGCTGGCGCCACAGAGGGGTCCGTCGCTCGG	2760
Ds	2706	TCATCTGCGCAGCTGTGAGCTTTGCTGGCGCCACAGAGGGGTCCGTCGCTCGG	2765
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Qy	2821	GACACTGGGCATCTCTCTGCTGCTGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2880
Ds	2826	GACACTGGGCATCTCTCTGCTGCTGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2885
Qy	2881	TGGCCACCTCTGCTGCGGGCTCTCTCCCTCATGGCACCTGGCCCTGGGGTCCGCCA	2940
Ds	2886	TGGCCACCTCTGCTGCGGGCTCTCTCCCTCATGGCACCTGGCCCTGGGGTCCGCCA	2945
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Ds	2946	CGCTCTCAGAGCTCCCGCTGGCTCGAGCCAGCTTCTGGACCTCCACCTCAGACTCA	3005
Qy	3001	GAGCCCTCTGCTCAGGAGACCTCTGCTGCTGAGCCAGACCCCTGCTCCCTCTCTCT	3060
Ds	3006	GAGCCCTCTGCTCAGGAGACCTCTGCTGCTGAGCCAGACCCCTGCTCCCTCTCTCT	3065
Qy	3061	TCTGAGGAAGGGGTAGGACTGGCCCGCAGAGCCCTGTGAGCCAGGCTGAGGCTACCGC	3120
Ds	3066	TCTGAGGAAGGGGTAGGACTGGCCCGCAGAGCCCTGTGAGCCAGGCTGAGGCTACCGC	3125
Qy	3121	ACTGGAGAGCCCCACAGGCTCAGGGGCTGGCCCTGGCCCTGGCCCTGGCCCTGGCCCTG	3180
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Qy	3181	GAGATGGTCTTATGGCTGCCATGGCTCTGGCACAGTCCAGTGGAGCCAGGAGAGGC	3240
Ds	3186	GAGATGGTCTTATGGCTGCCATGGCTCTGGCACAGTCCAGTGGAGCCAGGAGAGGC	3245
Qy	3241	ACAGGGGTCTCA 3252	
Ds	3246	ACAGGGGTCTCA 3257	
RESULT 2			
AAZ87712			
CD	AAZ87712 standard; DNA; 3829 BP.		
XX	AAZ87712;		
AC	AAZ87712;		
XX	19-MAY-2000 (first entry)		
XX	Human ESK1 (hESK1) protein encoding DNA.		
DE	ESK1; eag similar K+ channel; potassium channel associated disorder;		
KW	neurological; Alzheimer's disease; anxiety; panic; autism; hyperactivity;		
KW	obsessive-compulsive disorder; schizophrenia; Huntington's disease;		
KW	epilepsy; cardiovascular; musculoskeletal; proliferative; cancer;		
KW	ESK channel blocker; norepinephrine; neuroprotective; antidepressant;		
KW	tranquilizer; neuroleptic; antiParkinsonian; cardiac; cytostatic;		
KW	anticonvulsant; ds.		
XX	Homo sapiens.		
OS	Homo sapiens.		
XX			
Key	Location/Qualifiers		
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FT	/*tag= a		
FT	/*product= *ESK1 protein*		
XX	W0200009534-A1.		
XX	24-FEB-2000.		
XX			
XX	13-AUG-1999; 99WO-US18556.		
XX			
PR	14-AUG-1999; 98US-0096570.		
XX	(ELAN-) ELAN PHARM INC.		
XX	Forsayeth JR, Zhao BB;		
PI	WPI: 2000-224270/19.		
XX	P-PSDB; AAV77738.		
XX			
PT	Novel eag similar potassium channel polypeptide useful for treating		
PT	various neurological, cardiovascular, musculoskeletal and proliferative		
PT	disorders		
XX	Claim 8; Fig 1A-E; 52pp; English.		
PS			
XX	This DNA encodes a eag similar K+ channel (ESK) polypeptide (hESK1). The		
CC	hESK1 protein can be expressed by standard recombinant methodology. The		
CC	ESK polypeptide, polynucleotides and antibodies are useful for treating		
CC	and diagnosing various potassium channel associated disorders such as		
CC	neurological disorders, e.g. Alzheimer's disease, depression, anxiety,		

CC panic, obsessive-compulsive disorders, attention deficit, epilepsy;
CC hyperactivity disorders, autism, schizophrenia, Huntington's disease and
CC Parkinson's disease, cardiovascular disorders, musculoskeletal disorders
CC and proliferative disorders such as cancer. The ESK polynucleotide is
CC also useful for synthesis of ESK and gene mapping. The polypeptide can be
CC used in an assay to identify molecules such as synthetic drugs,
CC antibodies, peptides or other molecules which have an effect on the
CC activity of the ESK channel.

XX Sequence 3829 BP: 650 A: 1302 C: 1202 G: 675 T: 0 other:

Query Match 100.0%; Score 3250.4; DB 21; Length 3829;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3251; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY : ATGCGGCGCATGGGGGCTCTCGGCGCTCAGAACCTTCGTGACACCATCGGTACG 60
DB ATGCGGCGCATGGGGGCTCTCGGCGCTCAGAACCTTCGTGACACCATCGGTACG 304
QY 61 CGCTTCGACGCGACACAGTAACCTTCGTGCGCAACGCCAGGTGGGGCTCTTC 120
DB CGCTTCGACGCGACACAGTAACCTTCGTGCGCAACGCCAGGTGGGGGCTCTTC 364
QY 121 CCCGTGGTCTACTGCTGTATGGCTTCTGTGACCTACAGGGCTTCTCCGGGCTGAGGTC 180
DB CCCGTGGTCTACTGCTGTATGGCTTCTGTGACCTACAGGGCTTCTCCGGGCTGAGGTC 424
QY 181 ATGACGCGGGCTGTGCTGCTCTCTCTTTATGGCCACACACAGTGTAGCTCTCCGC 240
DB ATGACGCGGGCTGTGCTGCTCTCTCTTTATGGCCACACACAGTGTAGCTCTCTCCGC 484
QY 241 CAACAGATCCGCAAGGCGCTGGAGGACACAAAGATTTCAAGGCTGAGGTGATCTGTATAC 300
DB CAACAGATCCGCAAGGCGCTGGAGGACACAAAGATTTCAAGGCTGAGGTGATCTGTATAC 544
QY 301 CGGAAGACGGGCTCCCGTCTCTGTGCTCTCTGATGTATACCCATAAGAAATGAGAAA 360
DB CGGAAGACGGGCTCCCGTCTCTGTGCTCTCTGATGTATACCCATAAGAAATGAGAAA 604
QY 361 GGGGAGTGGCTCTCTCTAGTCTCTCAAGAGACATACGGAACCAAGAACCGAGG 420
DB GGGGAGTGGCTCTCTCTAGTCTCTCAAGAGACATACGGAACCAAGAACCGAGG 664
QY 421 GCGCCGACACATGAGAGGACAGGTGGTGGCGGCGCGATATGCGCGGACGATCC 480
DB GCGCCGACACATGAGAGGACAGGTGGTGGCGGCGCGATATGCGCGGACGATCC 724
QY 481 AAAGGCTTCAATGCGCAACGCGCGGAGCGGCGCTGTCTACCACTGTCTCGGCGAC 540
DB AAAGGCTTCAATGCGCAACGCGCGGAGCGGCGCTGTCTACCACTGTCTCGGCGAC 764
QY 541 CTGCAAGACGCGCCNAGGCGACGACACACATGAGGGGTGTTGGGAGAAACCA 600
DB CTGCAAGACGCGCCNAGGCGACGACACACATGAGGGGTGTTGGGAGAAACCA 844
QY 601 AACTTGGCTGAGTACAAAGTAGCCGCCATCGGGAAGTCGCCCTTCATCTGTGTCAGCTGT 660
DB AACTTGGCTGAGTACAAAGTAGCCGCCATCGGGAAGTCGCCCTTCATCTGTGTCAGCTGT 904
QY 661 GGGGACCTGAGAGCCACTGGGATGGCTTCACTGCTGCGCACACTCATG:GGGTGTC 720
DB GGGGACCTGAGAGCCACTGGGATGGCTTCACTGCTGCGCACACTCATG:GGGTGTC 964
QY 721 ACTGTGCGCTTACAGGCTGTGTGAGCACACGAGGAGCCAGTGGCGCGCGCGCG 780
DB ACTGTGCGCTTACAGGCTGTGTGAGCACACGAGGAGCCAGTGGCGCGCGCGCGCG 1024
QY 781 CCCAGCGTCTGTGACCTGGCGGTGAGGTCTCTTCACTTGTGACATGTGCTGAATTC 840
DB CCCAGCGTCTGTGACCTGGCGGTGAGGTCTCTTCACTTGTGACATGTGCTGAATTC 1084
QY 841 CCTACACACATCTGTGTCACGTCGGGCGAGGTGGTGTTCGCCCAAGTCCATTCGCTC 900
DB CCTACACACATCTGTGTCACGTCGGGCGAGGTGGTGTTCGCCCAAGTCCATTCGCTC

1085 CGTACCACATTCGTGCTCCAGTGGGCGCAGGTGGTGTTCGCCCAAGTCCATTCGCTC 1144
QY 901 CACTAGTCCACCACTGGTTCCTGTGTTGATGTCATCGACGCGCTCCCTTTACGCTGCTA 960
DB CACTAGTCCACCACTGGTTCCTGTGTTGATGTCATCGACGCGCTCCCTTTGACCTGCTA 1204
QY 961 CATGCCCTCAAGGTCACAGTGTACTTCGGGGGCCCACTGCTGACAGAGTGGGCTGCTG 1020
DB CATGCCCTCAAGGTCACAGTGTACTTCGGGGGCCCACTGCTGACAGAGTGGGCTGCTG 1264
QY 1021 CGCTGCTGCGCTGCTTCGGGGCTGGACCGGTACTCGCAGTACAGGCGCGCTGCTGCTG 1080
DB CGCTGCTGCGCTGCTTCGGGGCTGGACCGGTACTCGCAGTACAGGCGCGCTGCTGCTG 1324
QY 1081 ACAGTGTCTATGCGCTGTTCGCCCTGCTCGCGACACAGTGGTGGCTGCTGCTGCTGCTTAC 1140
DB ACAGTGTCTATGCGCTGTTCGCCCTGCTCGCGACACAGTGGTGGCTGCTGCTGCTGCTTAC 1384
QY 1141 ATTGGCCAGCGGAGATCGAGAGCAGCAATCCGAGCTGCCGTGAGATGGGTGGCTGCGAG 1200
DB ATTGGCCAGCGGAGATCGAGAGCAGCAATCCGAGCTGCCGTGAGATGGGTGGCTGCGAG 1444
QY 1201 GAGTGGCGCGCGACTGGAGACTCCCTACTACTGCTGGTGGCGCGGAGGCCAGCTGGAGGG 1260
DB GAGTGGCGCGCGACTGGAGACTCCCTACTACTGCTGGTGGCGCGGAGGCCAGCTGGAGGG 1504
QY 1261 AACAGCTCCGGCCAGAGTGACAACTCGACAGCAGCAGCGAGGCCAACGCGAGCGGGGTG 1320
DB AACAGCTCCGGCCAGAGTGACAACTCGACAGCAGCAGCGAGGCCAACGCGAGCGGGGTG 1564
QY 1321 GAGTGTGTGGGGCGCGCTGCTGGGAGGGCTACTACCTCCCTCTACTTCGCACTC 1380
DB GAGTGTGTGGGGCGCGCTGCTGGGAGGGCTACTACCTCCCTCTACTTCGCACTC 1624
QY 1381 AGCAGCTCCACAGCGTGGGCTTCGGCAACAGTCTCCGCCAACACGAGCACCCGAGAGATC 1440
DB AGCAGCTCCACAGCGTGGGCTTCGGCAACAGTCTCCGCCAACACGAGCACCCGAGAGATC 1684
QY 1441 TTCTCCATCTGACCATGTCTCATCGGCGCGCTGATCCAGCGGTGGTGTGGGAGCGTG 1500
DB TTCTCCATCTGACCATGTCTCATCGGCGCGCTGATCCAGCGGTGGTGTGGGAGCGTG 1744
QY 1501 ACGGCCATCATCAGCGCATGTAGCGCGCGCGCTTCTGTACACAGCGCACCGCGAC 1560
DB ACGGCCATCATCAGCGCATGTAGCGCGCGCGCTTCTGTACACAGCGCACCGCGAC 1804
QY 1561 CTGCGGACTACATCCGATCCACCGGTATCCCAAGCGCGCTCAAGCAGCGCATGTGGAG 1620
DB CTGCGGACTACATCCGATCCACCGGTATCCCAAGCGCGCTCAAGCAGCGCATGTGGAG 1864
QY 1621 TACTTCAGGCGCACTGGCGGTGACAAATGGCATCGACACCGAGCTGCTGAGAGC 1680
DB TACTTCAGGCGCACTGGCGGTGACAAATGGCATCGACACCGAGCTGCTGAGAGC 1924
QY 1681 CTCCCTGACGAGTGGCGGAGACATCGGCATCGACCTGCAAGAGAGTCTCTGAGCTG 1740
DB CTCCCTGACGAGTGGCGGAGACATCGGCATCGACCTGCAAGAGAGTCTCTGAGCTG 1984
QY 1741 CCACGTTTGGGCGCGCGCGCGGCTGCTGCGGGCACTGCTCTGCGCGCTGGCGCC 1800
DB CCACGTTTGGGCGCGCGCGCGGCTGCTGCGGGCACTGCTCTGCGCGCTGGCGCC 2044
QY 1801 GCCTTCTGCAAGCGCGGAGTACCTCATCCCAAGGCGGCTGCTGAGCGCTCTAC 1860
DB GCCTTCTGCAAGCGCGGAGTACCTCATCCCAAGGCGGCTGCTGAGCGCTCTAC 2104
QY 1861 TTGTCTGCTGCTGCTCCATCGAGGTGCTCAAGGGTGGACCGCTGCTCCCATCTAGGG 1920
DB TTGTCTGCTGCTGCTCCATCGAGGTGCTCAAGGGTGGACCGCTGCTCCCATCTAGGG 2164
QY 1921 AAGGGCACCTGATCGGCTGTGAGCTGCGCGCGGAGCAGGTGGTGAAGGCCAATGCC 1980
DB AAGGGCACCTGATCGGCTGTGAGCTGCGCGCGGAGCAGGTGGTGAAGGCCAATGCC 2224

CC neuroprotective and anticonvulsant activity. The hElk polypeptide can be
 CC used to screen for modulators of VGPCs, that are useful for treating
 CC abnormal ion flux disorders, CNS disorders such as migraines, hearing
 CC and vision problems, seizures, psychotic disorders and to prevent
 CC strokes. It can be used as a marker for diagnosis of diseases linked to
 CC this gene and also as reporter molecule in detection systems. The
 CC polynucleotide is useful for gene therapy, to rectify Elk expression.

XX Sequence 3249 BP: 562 A: 1097 C: 1000 G: 590 T: 0 other:

Query Match 99.8%; Score 3245.8; DB 21; Length 3249;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 3247; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGCGGGCCATCGGGGCTCTGGCGGCTCAGAACACCTTCCTGGACACACNTCGTAGG 60
 DB 1 ATGCGGGCCATCGGGGCTCTGGCGGCTCAGAACACCTTCCTGGACACACNTCGTAGG 60
 QY 61 CGCTTCGACGGCAGCACAGTAACCTTCGTGGCAACGCCAGGTGGCGGGCTCTTC 120
 DB 61 CGCTTCGACGGCAGCACAGTAACCTTCGTGGCAACGCCAGGTGGCGGGCTCTTC 120
 QY 121 CCGCTGCTACTGCTGATGGCTTCGTGACCTCAGGGCTTCCTCCGGGTGAGGTC 180
 DB 121 CCGCTGCTACTGCTGATGGCTTCGTGACCTCAGGGCTTCCTCCGGGTGAGGTC 180
 QY 181 ATGCAAGCGGGCTGCGCTGCTCTTATGGGCGACACACAGTGGCTGCTCCGC 240
 DB 181 ATGCAAGCGGGCTGCGCTGCTCTTATGGGCGACACACAGTGGCTGCTCCGC 240
 QY 241 CAACAGATCCGAGGGCCCTGGACGAGCACAAAGAGTTCAGGCTGAGCTGATCGTATC 300
 DB 241 CAACAGATCCGAGGGCCCTGGACGAGCACAAAGAGTTCAGGCTGAGCTGATCGTATC 300
 QY 301 CGGAAGAGCGGCTCCGCTCTGCTGCTCTGCTGATGATACCCATTAAGAGATGAGAA 360
 DB 301 CGGAAGAGCGGCTCCGCTCTGCTGCTCTGCTGATGATACCCATTAAGAGATGAGAA 360
 QY 361 GGGGAGGTGGCTCTCTTCTAGTCTCTCAAGAGACATCAGCGAAACCAAGACCGAGGG 420
 DB 361 GGGGAGGTGGCTCTCTTCTAGTCTCTCAAGAGACATCAGCGAAACCAAGACCGAGGG 420
 QY 421 GSCCGGACAGATGGAAGAGACAGGTGGTGGCGGCGCGGATATGCGCGGACAGATCC 480
 DB 421 GSCCGGACAGATGGAAGAGACAGGTGGTGGCGGCGCGGATATGCGCGGACAGATCC 480
 QY 481 AAAGGCTTCAATGCAATGCGGCGGAGGCGCGGCTGCTACCACTCTGCGGCGAC 540
 DB 481 AAAGGCTTCAATGCAATGCGGCGGAGCGGCGGCTGCTACCACTCTGCGGCGAC 540
 QY 541 CTGCAAGACCGCCCAAGGGGACGACAAAGCTCAATGAAGGGGTGTTGGGGAAGACCA 600
 DB 541 CTGCAAGACCGCCCAAGGGGACGACAAAGCTCAATGAAGGGGTGTTGGGGAAGACCA 600
 QY 601 AACTTGCCTGAGTACAAAGTAGCGGCCATCCGGAATCGGCCCTTCATCCCTGTGCACTGT 660
 DB 601 AACTTGCCTGAGTACAAAGTAGCGGCCATCCGGAATCGGCCCTTCATCCCTGTGCACTGT 660
 QY 661 GGGGACACTGAGACCACTGGGATGGCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 DB 661 GGGGACACTGAGACCACTGGGATGGCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 QY 721 ACTGTGCCCTACAGGCTGTGTGTGAGCACAGCGGAGCCAGTGTGCGCGCGGCGCG 780
 DB 721 ACTGTGCCCTACAGGCTGTGTGTGAGCACAGCGGAGCCAGTGTGCGCGCGGCGCG 780
 QY 781 CCGAGGCTGTGACCTGGCGGTGAGGCTCCTCTCTCATCTGTGACATGTGCTCAATTC 840
 DB 781 CCGAGGCTGTGACCTGGCGGTGAGGCTCCTCTCTCATCTGTGACATGTGCTCAATTC 840
 QY 841 CGTACCACATCGTGTCCAAAGTCGGGCGAGGTGTGTTGCGCCCAAGAGTCCATTCGCTC 900
 DB 841 CGTACCACATCGTGTCCAAAGTCGGGCGAGGTGTGTTGCGCCCAAGAGTCCATTCGCTC 900

QY 901 CACTACGTCACACACCTGGTTCCTGCTGATGTCATCGACGCTGCGCTTTCAGCTGCTA 960
 DB 901 CACTACGTCACACACCTGGTTCCTGCTGATGTCATCGACGCTGCGCTTTCAGCTGCTA 960
 QY 961 CATGCTTCAAGGTCACAGTGTACTGCGGGGCCATCTGCTGAAGAGCTGTGCGCTGCTG 1020
 DB 961 CATGCTTCAAGGTCACAGTGTACTGCGGGGCCATCTGCTGAAGAGCTGTGCGCTGCTG 1020
 QY 1021 CGCTGTGTGCGCTGCTTCCGCGCTGAGCGCTATCTCGAGTACAGCGCTGCTGCTG 1080
 DB 1021 CGCTGTGTGCGCTGCTTCCGCGCTGAGCGCTATCTCGAGTACAGCGCTGCTGCTG 1080
 QY 1081 ACAGTGTGCTGCGCGCTGCTGCGCTGCTGCGCTGCTGCGCTGCTGCTGCTGCTGCTG 1140
 DB 1081 ACAGTGTGCTGCGCGCTGCTGCGCTGCTGCGCTGCTGCGCTGCTGCTGCTGCTGCTG 1140
 QY 1141 ATTGGCAGCGGGAGATCGAGAGCAGGAATCGAGTTCGCTGAGATTCGCTGCTGCTG 1200
 DB 1141 ATTGGCAGCGGGAGATCGAGAGCAGGAATCGAGTTCGCTGAGATTCGCTGCTGCTG 1200
 QY 1201 GAGTGGCGCGCGCTGAGTTCCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
 DB 1201 GAGTGGCGCGCGCTGAGTTCCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
 QY 1261 AACAGCTCCGCGCGAGTGAACACTGAGCAGCAGCAGGCGGCGGCGGCGGCTG 1320
 DB 1261 AACAGCTCCGCGCGAGTGAACACTGAGCAGCAGCAGGCGGCGGCGGCGGCTG 1320
 QY 1321 GAGTGTGTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
 DB 1321 GAGTGTGTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
 QY 1381 AGCAGCTCACACAGCTGGGCTGCGCAAGCTGCTGCGCAAGCTGCTGCGCAAGCTGCTG 1440
 DB 1381 AGCAGCTCACACAGCTGGGCTGCGCAAGCTGCTGCGCAAGCTGCTGCGCAAGCTGCTG 1440
 QY 1441 TTCTCCATCTGACACCTGCTCATGCGCGCGCTGATGCGCGGCTGCTGCTGCTGCTGCTG 1500
 DB 1441 TTCTCCATCTGACACCTGCTCATGCGCGCGCTGATGCGCGGCTGCTGCTGCTGCTGCTG 1500
 QY 1501 AGGCGCATCATCAGCGCTGAGCGCGCGCTGAGCGCGCGCTGCTGCTGCTGCTGCTGCTG 1560
 DB 1501 AGGCGCATCATCAGCGCTGAGCGCGCGCTGAGCGCGCGCTGCTGCTGCTGCTGCTGCTG 1560
 QY 1561 CTGGCGCACTACATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
 DB 1561 CTGGCGCACTACATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
 QY 1621 TACTTCCAGCGCGCTGCGCGCTGAGCAATGGCATGACACACCGAGTGTGCTGCTGCTG 1680
 DB 1621 TACTTCCAGCGCGCTGCGCGCTGAGCAATGGCATGACACACCGAGTGTGCTGCTGCTG 1680
 QY 1681 CTGCTGACAGCTGCTGCGCGAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
 DB 1681 CTGCTGACAGCTGCTGCGCGAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
 QY 1741 CCACTGTTTGAAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
 DB 1741 CCACTGTTTGAAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
 QY 1801 GCTTCTGACCGCGCGGAGTACCTCATCCACCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
 DB 1801 GCTTCTGACCGCGCGGAGTACCTCATCCACCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
 QY 1861 TTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
 DB 1861 TTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
 QY 1921 AAGGCGACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
 DB 1921 AAGGCGACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980

Db	3061	TTCTAGGAAAGGGCTAGGACTGGGCGCCGACAGACCTGTGAGCCAGGCTGAGGCTACCGC	3120
Qy	3121	ACTGAGAGAGCCCCACACAGGCTCAGGGGGCTTGGCCCTTGGCCCTGGGACCCACAGGCTG	3180
Db	3121	ACTGAGAGAGCCCCACACAGGCTCAGGGGGCTTGGCCCTTGGCCCTGGGACCCACAGGCTG	3180
Qy	3181	GAGATGGTGCTTATTGGCTGCCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAGAGGC	3240
Db	3181	GAGATGGTGCTTATTGGCTGCCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAGAGGC	3240
Qy	3241	ACAGGGGTC 3249	
Db	3241	ACAGGGGTC 3249	
RESULT 4			
AA	AA14893		
ID	AA14893	standard; DNA; 3252 BP.	
XX	XX	AA14893;	
AC	XX		
CC	XX		
DI	XX	38-AUG-2000 (first entry)	
DE	XX	DNA encoding a herg4, potassium channel protein of the ERG family.	
KW	XX	Human; potassium channel protein; herg4; human erg related gene 4;	
KW	XX	epilepsy; migraine; cell proliferation disorder; cancer;	
KW	XX	comportmental trouble; neurotransmitter; hormone; ischemia;	
KW	XX	brain disease; cardiac disease; inflammation; pain; ss.	
CS	XX	Homo sapiens.	
Key	XX	Location/Qualifiers	
FT	XX	1..3252	
FI	XX	/*tag= a	
FI	XX	/product= "human erg related gene 4"	
XX	XX	W0200022001-A2.	
XX	XX	20-APR-2000.	
XX	XX	13-OCT-1999; 99WO-EP07671.	
XX	XX	13-OCT-1999; 98EP-0402540.	
XX	XX	(SNF1) SANOFI-SYNTHELABO.	
XX	XX	Renard S, Avenet P;	
XX	XX	WPI: 2000-317948/27.	
XX	XX	P-PSDB: AAY84835.	
XX	XX		
XX	XX	Novel herg4 polypeptide of human erg potassium channel family useful	
XX	XX	for treatment of epilepsy, migraine, cell proliferation	
XX	XX	Claim 5; Page 41-45; 48pp; English.	
XX	XX		
XX	XX	The present sequence encodes a human potassium channel protein of	
XX	XX	the ERG family, which is designated Herg4 (human erg related gene 4).	
XX	XX	The Herg4 polypeptides and polynucleotides are useful in the treatment	
XX	XX	of epilepsy, migraine, cell proliferation disorders, cancer,	
XX	XX	comportmental troubles, and to prevent or alter the effect of	
XX	XX	endogenous neurotransmitters and hormones. Antibodies against	
XX	XX	Herg4 are also useful for the treatment of cerebral, cardiac and renal	
XX	XX	ischemias, brain and cardiac diseases, inflammation, pain, and to mimic	
XX	XX	or antagonize the effect of endogenous neurotransmitters and hormones.	
XX	XX		
XX	XX	Sequence 3252 BP; 562 A; 1099 C; 1000 G; 591 T; 0 other;	
Query Match 99.8%; Score 3244; DB 21; Length 3252;			
Best Local Similarity 99.8%; Pred. No. 0;			
Matches 3247; Conservative 0; Mismatches 5; Indels 0; Gaps 0;			

XX	SQ Sequence 3857 BP; 677 A; 1301 C; 1201 G; 678 T; 0 other:									
SQ	Query Match									
	Best Loc.: Similarity 99.98; Pred. No. 0; Length 3857;									
	Matches 3244; Conservative 0; Mismatches 5; Indels 3; Gaps 2:									
QY	1	ATGCGGCGATGCGGGGCGCTCTGGGCGCTCAGAACACCTTCTGTGACACCATGCTACG	60							
DB	249	ATGCGGCGATGCGGGGCGCTCTGGGCGCGCACAAACACCTTCTGTGACACCATGCTACG	103							
QY	61	CGCTTCAGCGCAGCGACAGTAACCTTGGTCTGGCAAGCCGACAGTGGCGGGCTCTC	120							
DB	309	CGCTTCAGCGCAGCGACAGTAACCTTGGTCTGGCAAGCCGACAGTGGCGGGCTCTC	165							
QY	121	CCGCTGGCTACTGCTCTGATGGCTCTGTGACCTCAGCGCTTCGCCGGCTGAGTCTC	180							
DB	366	CCGCTGGCTACTGCTCTGATGGCTCTGTGACCTCAGCGCTTCGCCGGCTGAGTCTC	425							
QY	181	ATGCGGGGCGCTGCTGCTCTCTCTTTATGGCGCACACCATGAGTCTGCGG	240							
DB	426	ATGCGGGGCGCTGCTGCTCTCTTTATGGCGCACACCATGAGTCTGCTCGG	485							
QY	241	CAACAGATCCGCAAGGCGCTGGAGCGACACAAAGAGTTCAGGCTGAGCTGATCTGAC	300							
DB	486	CAACAGATCCGCAAGGCGCTGGAGCGACACAAAGAGTTCAGGCTGAGCTGATCTGAC	545							
QY	301	CGGAAGAGCGGCTCCCGTCTCTGTCTCTCTGGATGATACCCATAGAGATGAGAA	360							
DB	546	CGGAAGAGCGGCTCCCGTCTCTGTCTCTCTGGATGATACCCATAGAGATGAGAA	505							
QY	361	GGGAGGTGGCTCTCTCTCTAGTCTCTCAAGGACATCAGCGAAACCAAGACGAGG	420							
DB	606	GGGAGGTGGCTCTCTCTCTAGTCTCTCAAGGACATCAGCGAAACCAAGACGAGG	665							
QY	421	GGCCCGACATGGAAGGACAGGTGGCGCGCGGATGCGCGGACGATGCGCGGACATCC	480							
DB	666	GGCCCGACATGGAAGGACAGGTGGCGCGCGGATGCGCGGACGATGCGCGGACATCC	725							
QY	481	AAAGGCTTCAATGCAACCGCGCGGAGCGGGCGGTGCTTACCACTGTCGCGGAC	540							
DB	726	AAAGGCTTCAATGCAACCGCGCGGAGCGGGCGGTGCTTACCACTGTCGCGGAC	785							
QY	541	CTGCAGAGCGCCACAGGCAAGCAAGCTCAATAAGGGGTGTTGGGAGAAACCA	600							
DB	786	CTGCAGAGCGCCACAGGCAAGCAAGCTCAATAAGGGGTGTTGGGAGAAACCA	845							
QY	601	AACCTGCTGAGTACAAAGTAGCGGCAATCGGAAGTCGCCCTTCATCTGTTGCACTGT	660							
DB	846	AACCTGCTGAGTACAAAGTAGCGGCAATCGGAAGTCGCCCTTCATCTGTTGCACTGT	905							
QY	661	GGGGCACTGAGAGCACTGCGGATGGCTTATCTCTGCTCCACACTATGCGGTGTC	720							
DB	906	GGGGCACTGAGAGCACTGCGGATGGCTTATCTCTGCTCCACACTATGCGGTGTC	965							
QY	721	ACTGTSCCTACAGGCTGTGTGAGCACAGCGGAGCGCCAGTGGCGCGCGCGCG	780							
DB	966	ACTGTSCCTACAGGCTGTGTGAGCACAGCGGAGCGCCAGTGGCGCGCGCGCGCG	1025							
QY	781	CCCAGGCTCTGAGCTGGCGGTGAGTCTCTTCATCTCTGACATTTGCTGAATTC	840							
DB	1026	CCCAGGCTCTGAGCTGGCGGTGAGTCTCTTCATCTCTGACATTTGCTGAATTC	1085							
QY	841	CGTACACATCTGCTCCAACTCGGGCGAGGTGTGTTGCCCAAGTCCATTTGCCCTC	900							
DB	1086	CGTACACATCTGCTCCAACTCGGGCGAGGTGTGTTGCCCAAGTCCATTTGCCCTC	1145							
QY	901	CACCTAGTCAACACCTGCTCTGCTGATGTCAACACGCGTGGCTTTGACCTGCTA	960							
DB	1146	CACCTAGTCAACACCTGCTCTGCTGATGTCAACACGCGTGGCTTTGACCTGCTA	1205							
QY	961	CATGCTTCAAGGTCAAGCTGACTTGGGGGCCCATCTGCTGAGAGCGGTGGCGCTG	1020							

DB	1206	CATGCTTCAAGGTCAAGCTGACTTTCGGGGCGCCATCTGCTGAGAGAGCGTGGCGCTG	1265
QY	1021	CGCTTCTGCTGCTGCTTCCGCGGCTGACACCGGTACTCGAGTACACGCGGCTGCTG	1080
DB	1266	CGCTTCTGCTGCTGCTTCCGCGGCTGACACCGGTACTCGAGTACACGCGGCTGCTG	1325
QY	1081	ACACTGCTCATGCGCGTGTTCGCCCTGCTCGGCGACTGGTGGCTGCTGCTGTTTAC	1140
DB	1326	ACACTGCTCATGCGCGTGTTCGCCCTGCTCGGCGACTGGTGGCTGCTGCTGTTTAC	1385
QY	1141	ATTGGCCAGCGGAGATCGAGAGACAGCAATCCGAGTTCGCTGAGATGGCTGCTGAG	1200
DB	1386	ATTGGCCAGCGGAGATCGAGAGACAGCAATCCGAGTTCGCTGAGATGGCTGCTGAG	1445
QY	1201	GAGCTGGCGCGCGGACTGGAGACTCCCTACTACCTTGGTGGCGGAGGACGCTGAGGG	1260
DB	1446	GAGCTGGCGCGCGGACTGGAGACTCCCTACTACCTTGGTGGCGGAGGACGCTGAGGG	1505
QY	1261	AACAGCTCCGGCCAGAGTGACAACTGACAGCAGCAGCGAGCGCAACGAGCGGCGTG	1320
DB	1506	AACAGCTCCGGCCAGAGTGACAACTGACAGCAGCAGCGAGCGCAACGAGCGGCGTG	1565
QY	1321	GAGCTGCTGGGGGCGCGCTGCTGCGCAGCGGCTTACATCACTCCCTTACTTCCGACTC	1380
DB	1566	GAGCTGCTGGGGGCGCGCTGCTGCGCAGCGGCTTACATCACTCCCTTACTTCCGACTC	1625
QY	1381	AGCAGCTCACACGCGTGGCTTGGCAACGCTGTCGGCAACACAGGACACGAGCAAGATC	1440
DB	1626	AGCAGCTCACACGCGTGGCTTGGCAACGCTGTCGGCAACACAGGACACGAGCAAGATC	1685
QY	1441	TTCGATCTGACCATGCTCATGCGGCGCTGATGACGCGGCTGTTTGGGAACTG	1500
DB	1686	TTCGATCTGACCATGCTCATGCGGCGCTGATGACGCGGCTGTTTGGGAACTG	1745
QY	1501	ACGGCATCAICAGCGCATGTACGCGCGCGCTTCTGTACACAGCGCGCACGCGGAC	1560
DB	1746	ACGGCATCAICAGCGCATGTACGCGCGCGCTTCTGTACACAGCGCGCACGCGGAC	1805
QY	1561	CTGGGCGATACATCGCATCCACCGCTATCCCGCAGCGCTCAAGCAGCGGATGCTGAG	1620
DB	1806	CAGCGGAGCTACATCCGATCCACCGCTATCCCGCAGCGCTCAAGCAGCGGATGCTGAG	1865
QY	1621	TACTTCCAGCGCACCTGGCGGTGAACATGTCATCGACACACCGAGCTGCTGACAGC	1680
DB	1866	TACTTCCAGCGCACCTGGCGGTGAACATGTCATCGACACACCGAGCTGCTGACAGC	1925
QY	1681	CTCCCTGACAGCTGCGCGGACATCGCCATGACCTGTCACAGAGGAGTCTTCCAGCTG	1740
DB	1926	CTCCCTGACAGCTGCGCGGACATCGCCATGACCTGTCACAGAGGAGTCTTCCAGCTG	1985
QY	1741	CCACTGTTTCCAGCGCGCGGCTGCTGCGGCGACTGCTCTTGGCGCTGCGGCGC	1800
DB	1986	CCACTGTTTCCAGCGCGCGGCTGCTGCGGCGACTGCTCTTGGCGCTGCGGCGC	2045
QY	1801	GCTTCTGACGCGCGGCGGAGTACCTTCATCCAGCGGATGCGCTGACAGGCGCTTAC	1860
DB	2046	GCTTCTGACGCGCGGCGGAGTACCTTCATCCAGCGGATGCGCTGACAGGCGCTTAC	2105
QY	1861	TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGTGGCACCGTCTCGCCATCTAGGG	1920
DB	2106	TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGTGGCACCGTCTCGCCATCTAGGG	2165
QY	1921	AAGGGCGACCTGATGCGCTGTGAGTGGCGCGCGGAGGAGGAGGTTAAAGGCGCAATGCC	1980
DB	2166	AAGGGCGACCTGATGCGCTGTGAGTGGCGCGCGGAGGAGGAGGTTAAAGGCGCAATGCC	2225
QY	1981	GAGCTGAAGGGGCTGAGCTACTGCGCTGCTGAGTGTCTGACAGCTGGCTGGCTTCCACAC	2040
DB	2226	GAGCTGAAGGGGCTGAGCTACTGCGCTGCTGAGTGTCTGACAGCTGGCTGGCTTCCACAC	2285
QY	2041	AGCTTCCGCTGTACCCCGAGTTTGGCGCGCGCTTCACTGCTGGCGCTCCGAGGGGAGCTC	2100
DB	2286	AGCTTCCGCTGTACCCCGAGTTTGGCGCGCGCTTCACTGCTGGCGCTCCGAGGGGAGCTC	2345

QY	2101	AGCTAAACCTGGGTGGGGAGGCTCTGCAGAGGTGCACACAGCTCCCTGAGCGGC	2163
DB	2346	AGCTAAACCTGGGTGGGGAGGCTCTGCAGAGGTGCACACAGTCCCTGAGCGGC	2405
QY	2161	GACAAATACCCCTATGTCACAGCTGGAGGAGGAGACAGATAGGGAGCAGGGCCCAACG	2220
DB	2406	GACAAATACCCCTATGTCACAGCTGGAGGAGGAGGAGACAGATGGGAGCAGGGCCCAACG	2465
QY	2221	GTCTCCCAAGCCCAAGCTGATGAGCCCTCCAGCCCCCTGCTGTCCCTTGGGTGCACCTCC	2280
DB	2466	GTCTCCCAAGCCCAAGCTGATGAGCCCTCCAGCCCCCTGCTGTCCCTTGGGTGCACCTCC	2525
QY	2281	TCATCCTCAGCTGCACAGCTGCTATCCDCAAGCTGCAGACAGACCCCGGCTCGTCTAGGT	2340
DB	2526	TCATCCTCAGCTGCACAGCTGCTATCCDCAAGCTGCAGACAGACCCCGGCTCGTCTAGGT	2585
QY	2341	GGCAGAGGAGGCCAGGACAGGCCAGGGGCTTTGAAGGCTGAGGCTGGCCCCCTCTGCTCC	2400
DB	2586	GGCAGAGGAGGCCAGGACAGGCCAGGGGCTTTGAAGGCTGAGGCTGGCCCCCTCTGCTCC	2645
QY	2401	CCACGGGCCCTAGAGGGCTACGGCTGCCCCCCCATGCCATGAATGTGCCCCCCAGATCTG	2460
DB	2646	CCACGGGCCCTAGAGGGCTACGGCTGCCCCCCCATGCCATGAATGTGCCCCCCAGATCTG	2705
QY	2461	AGCCCCAGGGTAGTAGATGGCGATTGAAGACGGCTGGGCTGGACACAGCCCAAGTCTCT	2520
DB	2706	AGCCCCAGGGTAGATAGATGGCATTTGAAGACGGCTGGGCTGGACACAGCCCAAGTCTCT	2765
QY	2521	TTCCGCTGGGCCAGTCTGGCCGGGAATGTATCAGACAGCCCTCCCTCTGGACACAGAGCC	2580
DB	2766	TTCCGCTGGGCCAGTCTGGCCGGGAATGTATCAGACAGCCCTCCCTCTGGACACAGAGCC	2825
QY	2581	GGCTGCTCACTGTTCCCAATGGGCCACAGCGGCAAGGCAAGACACAGACACTGACCAAG	2640
DB	2826	GGCTGCTCACTGTTCCCAATGGGCCACAGCGGCAAGGCAAGACACAGACACTGACCAAG	2885
QY	2641	CTTCGGCAGGGGTGACAGAGCTGTGACAGACAGTCTCGGACTTGCACATGGGGAGAGACTCG	2700
DB	2886	CTTCGGCAGGGGTGACAGAGCTGTGACAGACAGTCTCGGACTTGCACATGGGGAGAGACTCG	2945
QY	2701	TCACTTCGCCAGGCTGTGACACTTGTCTTGGGCCCCACAGAGGAGGGTCCGTGGCCCTCG	2760
DB	2946	TCACTTCGCCAGGCTGTGACACTTGTCTTGGGCCCCACAGAGGAGGGTCCGTGGCCCTCG	3005
QY	2761	GCATGGGAGAGGGCCGCTGCCACGACAGCACTTCGGGACTTCTGCAGGCTCTGTGCTG	2820
DB	3006	GCATGGGAGAGGGCCGCTGCCACGACAGCACTTCGGGACTTCTGCAGGCTCTGTGCTG	3065
QY	2821	GACACTGGGGCATCTCTCTACTGTGCTGCAGCCCCCAGCTTGGCTCTGTCTTGAAGTGGACT	2880
DB	3066	GACACTGGGGCATCTCTCTACTGTGCTGCAGCCCCCAGCTTGGCTCTGTCTTGAAGTGGACT	3125
QY	2881	TGGCCCCACCTCTGTCGGGGCCCTCCCTCTCAAGCACCTTGGCCCTGGGCTGGGCTCCCA	2940
DB	3126	TGGCCCCACCTCTGTCGGGGCCCTCCCTCTCAAGCACCTTGGCCCTGGGCTGGGCTCCCA	3185
QY	2941	GGGTCTCAGAGCTCCCTTGGCCCTCGAGCCACAGCTTTCTTGGACCTCCACCTCAGACTCA	3000
DB	3186	GGGTCTCAGAGCTCCCTTGGCCCTCGAGCCACAGCTTTCTTGGACCTCCACCTCAGACTCA	3245
QY	3001	GAGCCCCCTGCTCAGGAGACTCTGTCTGTAGCCACAGCACCCCTGCCTCCCTCTCTCT	3060
DB	3246	GAGCCCCCTGCTCAGGAGACTCTGTCTGTAGCCACAGCACCCCTGCCTCCCTCTCTCT	3305
QY	3061	TTCTAGGAAGAGGGCTAGACTTGGGCCCGCAGAGCCCTGTGCAGCAGGCTGAGGCTACCAAGC	3120
DB	3306	TTCTAGGAAGAGGGCTAGACTTGGGCCCGCAGAGCCCTGTGCAGCAGGCTGAGGCTACCAAGC	3365
QY	3121	ACTGGAGAGCCCCACACAGGCTCAGGGGGCTTGGCTTGCCTTGGGACCCCCACAGCTG	3180
DB	3366	ACTGGAGAGCCCCACACAGGCTCAGGGGGCTTGGCTTGGGAGCCCCACAGCTG	3425

Qy	3181	GAGATGGTGCTTATTTGGCTGCCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAGAGGC	3244
Db	3426	GAGATGGTGCTTATTTGGCTGCCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAGAGGC	3485
Qy	3241	ACAGGGGCTCTGA	3252
Db	3486	ACAGGGGCTCTGA	3497
RESULT 6			
Id	AAZ50452		
	AAZ50452 standard; cDNA; 3355 BP.		
AC	AAZ50452;		
DT	18-MAY-2000 (first entry)		
XX	Monkey potassium channel molecule ERG-LP1 cDNA.		
Df	Monkey; potassium channel molecule; ERG-like protein 1; ERG-LP1;		
Kw	neuroprotective; antiParkinsonian; anticonvulsant; antidepressant;		
Kw	neuroleptic; nootropic; treatment; CNS disorder; central nervous system;		
Kw	potassium channel mediated disorder; epilepsy; Alzheimer's disease;		
Kw	Parkinson's; multiple sclerosis; depression; schizophrenia; amnesia; ss.		
XX	Primates.		
XX			
Fh	Key	Location/Qualifiers	
FT	5 UTR	1..103	
FT		/*tag= a	
FT	CDS	104..3455	
FT		/*tag= b	
FT		/*product= "ERG-LP1"	
FT		/note= "This region is specifically claimed"	
XX			
FN	W0200005346-A1.		
XX			
PD	03-FEB-2000.		
XX			
PF	21-JUL-1999;	99WO-US:6752.	
XX			
PR	21-JUL-1998;	98US-0119855.	
XX			
PA	(MILL-) MILLENNIUM PHARM INC.		
XX			
PL	Curtis RAZ;		
XX			
DR	WP1: 2000-182682/16.		
XX	P-PSDB: AAY44904.		
PT	Novel gene encoding potassium channel molecule useful in treating		
PT	central nervous system disorders such as Alzheimer's disease, multiple		
PT	sclerosis, and schizophrenia		
PS	Claim 2: Fig 1: 144pp; English.		
XX			
CC	The present sequence is a cDNA encoding ERG-like protein 1 (ERG-LP1)		
CC	which is a member of ERG potassium channel family. This sequence is		
CC	from a full length clone jlkpa25d10 which was derived from monkey		
CC	hippocampal library. ERG-LP1 is expressed exclusively in the brain.		
CC	Highest expression is found in cortical regions, hippocampus, caudate		
CC	and amygdala. The protein functions as a potassium channel modulator and		
CC	has neuroprotective, antiParkinsonian, anticonvulsant, antidepressant,		
CC	neuroleptic and nootropic activities. The present sequence is		
CC	useful for treating several potassium channel mediated disorders (CNS		
CC	disorders) such as Alzheimer's disease, Parkinson's disease, multiple		
CC	sclerosis, epilepsy, depression, schizophrenic disorders and amnesia.		
XX			
SQ	Sequence 3355 BP; 580 A; 1128 C; 1041 G; 606 T; 0 other;		
Query Match	97.0%; Score 3156; DB 21: Length 3355;		
Best Local Similarity	98.2%; Pred. No. 0;		
Matches 3192: Conservative	0; Mismatches 60; Indels 0; Gaps 0;		

QY 1 ATGCGGCGCATGCGGGGCTCTGTCGCGCTCAGAACACCTTCCTGCACACCATCGTAGC 60
DB 104 ATGCGGCGCATGCGGGGCTCTGTCGCGCTCAGAACACCTTCCTGCACACCATCGTAGC 163
QY 61 CGCTTCGAGCGCACACAGTAACCTTCGTCGGGCAACCCGAGGTGGCGGGCTCTTC 220
DB 164 CGCTTCGAGCGCACACAGTAACCTTCGTCGGGCAACCCGAGGTGGCGGGCTCTTC 223
QY 121 CCGCTGGCTACTGCTCTGATGGCTTCTGTGACCTACGGGCTCTTCGCGGGCTGAGGTC 180
DB 224 CCGCTGGCTACTGCTCTGATGGCTTCTGTGACCTACGGGCTCTTCGCGGGCTGAGGTC 283
QY 181 ATGCAGCGGGCTGTGCTGCTCTCTCTCTTTATGGCCACACACAGTAGCTGCTCCGC 240
DB 284 ATGCAGCGGGCTGTGCTGCTCTCTCTTTATGGCCACACACAGTAGCTGCTCCGC 343
QY 241 CAACAGATCCGCAAGGCGCTGGACGAGCACAAAGGATTCAGGCTGAGCTGATCTGTAC 300
DB 344 CAACAGATCCGCAAGGCGCTGGACGAGCACAAAGGATTCAGGCTGAGCTGATCTGTAC 403
QY 301 CGGAAGAGCGGGCTCCGCTCTGCTGCTCTCTGATGTGATACCCATAAAGATGAGAAA 360
DB 404 CGGAAGAGCGGGCTCCGCTCTGCTGCTCTCTGATGTGATACCCATAAAGATGAGAAA 463
QY 361 GGGGAGGTGGCTCTCTCTCTCTCAAGAGACATCAGCGAAACCAAGAACCGAGGG 420
DB 464 GGGGAGGTGGCTCTCTCTCTCTCAAGAGACATCAGTCAAAACCAAGAACCGAGGG 523
QY 421 GCGCCGACACATGGAAGGACACAGGTGGTGGCGGCGCGGATATGGCGGGCACGATCC 480
DB 524 GCGCCGACACATGGAAGGACACAGGTAGTGGCGGCGCGGATATGGCGGGCACGATCC 583
QY 481 AAAGGCTTCAATGCCAACCGCGCGGAGCGGCGCTGCTTACCACTGTCCGGGCAC 540
DB 584 AAAGGCTTCAATGCCAACCGCGCGGAGCGGCGCTGCTTACCACTGTCCGGGCAC 643
QY 541 CTGCAGAGACGCCCAAGGGCAAGCACAAAGCTCAATAAGGGGGTGTGGGAGAAACCA 500
DB 644 CTGCAGAGACGCCCAAGGGCAAGCACAAAGCTCAATAAGGGGGTGTGGGAGAAACCA 703
QY 601 AACTTGCCTGAGTACAAAGTAGCCGCTATCGGAAGTCCGCCCTTCATCCTGTTGCACCTGT 560
DB 704 AACTTGCCTGAGTACAAAGTAGCTGCCATCGGAAGTCCGCTTCATCCTGTTGCACCTGT 763
QY 661 GGGGCACTGAGAGCGACCTGGGATGGCTTATCTGCTCGCCACACTCAATGAGCTGTC 720
DB 764 GGGGCGCTGAGGGCACCTGGGATGGCTTATCTGCTCGCCACACTCAATGAGCTGTC 823
QY 721 ACTGTGCGCTACAGCGTGTGTGAGCACAGCAGCGGAGCCCAAGTGTGCGGCTGCGCGG 780
DB 824 ACCGTGCGCTACAGCGTGTGTGAGCACAGCAGCGGAGCCCAAGTGTGCGGCTGCGCGG 883
QY 781 CCGACGCTGTGACCTGGCGGTGGAGTCTCTTTCATCTGATCTGACATGTGCTGATTTTC 840
DB 884 CCGACGCTGTGACCTGGCGGTGGAGTCTCTTTCATCTGATCTGACATGTGCTGATTTTC 943
QY 841 CGTACACATCTGTTCCAACTCGGGGCGAGTGGTGTGTGCCCAAGAGTCCATTCGCTC 900
DB 944 CGTACACATCTGTTCCAACTCGGGGCGAGTGGTGTGTGCCCAAGAGTCCATTCGCTC 1003
QY 901 CACTACGTACACACCTGGTCTCTGCTGATGTATGCGAGCGGTGGCGCTTGTACCTGCTA 960
DB 1004 CACTACGTACACACCTGGTCTCTGCTGATGTATGCGAGCGGTGGCGCTTGTACCTGCTA 1063
QY 961 CATGCTTCAAGTCAAGCTGTACTTGGGGGCCCATCTGCTGAAGAGGTTGGCGCTGCTG 1020
DB 1064 CATGCTTCAAGTCAAGCTGTACTTGGGGGCCCATCTGCTGAAGAGGTTGGCGCTGCTG 1123
QY 1021 CGCGCTGCTGCGCTCTCTCGCGGCTGGACCGGTACTCGAGTACAGCGCGGTGGTGGT 1080
DB 1124 CGCGCTGCTGCGCTCTCTCGCGGCTGGACCGGTACTCGAGTACAGCGCGGTGGTGGT 1183

QY 1081 ACAGTGTCTATGCGCGCTGTGCGCTGCTGCGGCACTGCGTCTGCGCTGCGCTGCGTCTTAC 1140
DB 1184 ACAGTGTCTATGCGCGCTGTGCGCTGCTGCGGCACTGCGTCTGCGCTGCGTCTTAC 1243
QY 1141 ATTGGCAGCGGGAGATCCAGACAGCAATCCGAGCTGCTGAGATGGCTGCGTCTGAG 1200
DB 1244 ATTGGCAGCGGGAGATCCAGACAGCAATCCGAGCTGCTGAGATGGCTGCGTCTGAG 1303
QY 1201 GAGTGGCGCGCGAGTGGAGACTCCCTACTACCTGGTGGGCGGAGCGCCAGCTGAGGG 1260
DB 1304 GAGTGGCGCGCGAGTGGAGACTCCCTACTACTTGGTGGGCGGAGACACCGGAGGG 1363
QY 1361 AACAGTCCGCGCAGAGTGCACACAGCAGCAGCGAGGGCCAAAGGAGCGGGGCTG 1320
DB 1364 AACAGTCTGGCAGAGTGCACACAGCAGCAGCGAGGGCCAAAGGAGCGGGGCTG 1423
QY 1321 GAGTGTGCGCGCGCGCTGCTGCGCAGCGCTACATACCTGCTCTACTTGCACCTC 1380
DB 1424 GAGTGTGCGCGCGCGCTGCTGCGCAGCGCTACATACCTGCTCTACTTGCACCTC 1483
QY 1381 AGCAGCTCAGCAGCGTGGCTTGGCAGAGTGTCCGCAACAGCAGCGACCGAGAGATC 1440
DB 1484 AGCAGCTCAGCAGCGTGGCTTGGCAGAGTGTCCGCAACAGCAGCGACCTGAGAGATC 1543
QY 1441 TTCTCCATCTGCACCACTGCTCATCGCGCGCTGATGCACCGGCTGTGTTGGAACTG 1500
DB 1544 TTCTCCATCTGCACCACTGCTCATCGCGCGCTGATGCACCGGCTGTGTTGGAACTG 1603
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QY 1561 CTGCGCACTACATCTCGCATCCACCTATCCCAAGCCCTCAAGCAGCGCTGCTGGAG 1620
DB 1664 CTGCGCACTACATCTCGCATCCACCTATCCCAAGCCCTCAAGCAGCGCTGCTGGAG 1723
QY 1621 TACTTCAGCGCACTTGGCGGCTGACATGCAATGCACTGCACACAGCGAGTCTGAGAGC 1680
DB 1724 TACTTCAGCGCACTTGGCGGCTGACATGCAATGCACTGCACACAGCGAGTCTGAGAGC 1783
QY 1681 CTCCTTCAGCGCTGGCGGAGCATCGCATGCACTGCACAGAGGCTCTGAGAGTCTG 1740
DB 1784 CTCCTTCAGCGCTGGCGGAGCATCGCATGCACTGCACAGAGGCTCTGAGAGTCTG 1843
QY 1741 CCAGTGTGTAGCGGCGCGCGCTGCTGCGGGCACTGCTCTGGCGCTGGCGCC 1800
DB 1844 CCAGTGTGTAGCGGCGCGCGCTGCTGCGGGCACTGCTCTGGCGCTGGCGCC 1903
QY 1801 GCCTTCTGCACGCGCGGAGTACCTCATCCCAAGGCTGCGCTGCGAGGCGCTCTAC 1860
DB 1904 GCCTTCTGCACGCGCGGAGTACCTCATCCCAAGGAGTGCCTGCGAGGCGCTCTAC 1963
QY 1861 TTTGCTGCTCTGGCTCCATGAGAGTGTCAAGGGTGGCAGCGTCTGCGATCTAGGG 1920
DB 1964 TTTGCTGCTCTGGCTCCATGAGAGTGTCAAGGGTGGCAGCGTCTGCGATCTAGGG 2023
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DB 2024 AAGGGCACTGTAGGCTGTGAGCTGCGCGCGGAGCAGTGTGTAAGGCCAATGCC 2083
QY 1981 GAGCTGAAGGGCTGAGTACTGCTGCTGCAAGTGTGCACTGCTGCTGGCTGCGAGC 2040
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DB 2144 AGCTTCTGCTGTACCCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2203
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Db 2264 GACAATACCTTATGTCACGCTGGAGGAGAGAGACAGATGGGAGCAGGCGCCACCA 2323
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Db 2324 GTCTCCAGCCAGCTGATGAGCCCTCCAGCCCTGCTGTCCTCCCTGCTGCTGCTCC 2383
QY 2281 TCATCTCAGCTGCCAAGCTGCTATCCCTCCAGCTGGAACAGCAGCCCGCTGCTGCTAGGT 2340
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QY 2341 GCCAGAGGAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2400
Db 2444 GGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2503
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Db 2564 AGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2623
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Db 2624 TTCCGGCTGGGCGAGCTGTCGCGCGGAGTGTAGCAGCAGCCCTCCCTGGACAGCAGC 2633
QY 2581 GGCCTGCTACTGTTCCCATGGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2640
Db 2684 GGCCTGCTACTGTTCCCATGGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2743
QY 2641 CTTCGGCAGGCGGTACAGAGCTGTCAGCAGAGTGTGTCAGATGCGGAGGAGGAGTCCAG 2700
Db 2744 CTTCGGCAGGCGGTATGAGCTGTGACAGAGTGTGTCAGATGCGGAGGAGGAGTCCAG 2803
QY 2701 TCACCTTCGCGAGGCTGTGAGCTTGTCTGCGCGCCACAGGAGGAGGAGGAGGAGGAGG 2760
Db 2804 TCACCTTCGCGAGGCTGTGAGCTTGTCTGCGCGCCACAGGAGGAGGAGGAGGAGGAGG 2863
QY 2761 GCATCGGAGAGGCGGTGCCAGCAGCAGCTCCGCGCTCTGCAAGCTCTGCTGCTGCTG 2820
Db 2864 GCTCAGGAGAGGCGGTATGCCAGCAGCAGCTCCGCGCTCTGCAAGCTCTGCTGCTGCTG 2923
QY 2821 GACACTGGGGGCTCTCTACTGCTGCGCGCCACAGCTGCTGCTGCTGCTGCTGCTGCTG 2880
Db 2924 GACACTGGGGGCTCTCTACTGCTGCGCGCCACAGCTGCTGCTGCTGCTGCTGCTGCTG 2983
QY 2881 TGGCCCCAGCTCTGCGGGGCTCTCTCTCTCATGACACCTGCGCGCTGCGCGCTGCGCG 2940
Db 2984 TGGCCCCAGCTCTGCGGGGCTCTCTCTCTCATGACACCTGCGCGCTGCGCGCTGCGCG 3043
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QY 3061 TCTGAGGAGGGGCTAGGACTGGGCGCGCAGAGCTGTGAGCCAGGCTGAGGCTTACACAG 3120
Db 3164 TCTGAGGAGGGGCTAGGACTGGGCGCGCAGAGCTGTGAGCCAGGCTGAGGCTTACACAG 3223
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QY 3181 GAGATGGCTTATGGCTGCCATGCTCTGACAGTCCAGTGCAGCCAGGAGGAGGAGGAGG 3240
Db 3284 GAGATGGCTTATGGCTGCCATGCTCTGACAGTCCAGTGCAGCCAGGAGGAGGAGGAGG 3343
QY 3241 ACAGGGGCTCTGA 3252
|||||
```

```
Db 3344 ACAGGGGCTCTGA 3355
RESULT 7
AA84919
ID AAX84919 standard; DNA; 3715 BP.
XX
AC AAX84919;
XX
DT 28-SEP-1999 (first entry)
XX
DE Rat brain specific potassium channel protein coding sequence.
XX
KW Brain specific potassium channel; central nervous system disorder;
KW dementia; cerebral ischaemic sclerosis; therapy; probe; ss.
XX
OS Rattus sp.
XX
PN W09937677-A1.
XX
PU 29-JUL-1999.
XX
PF 20-JAN-1999; 99WO-JP00190.
PR 04-DEC-1998; 98JP-0346198.
PR 23-JAN-1998; 98JP-0011434.
XX
PA (YAMA ) YAMANOUCHI PHARM CO LTD.
XX
PI Miyake A, Mochizuki S, Yokoi H;
XX
WP1; 1999-458683/38.
XX
PT Potassium channel protein expressed specifically in brain tissue and
PT method for its production
XX
PS Example 3; Page 54-57; 63pp; English.
XX
CC This sequence encodes a rat potassium channel protein, and was used as a
CC probe to isolate DNA encoding the protein of the invention. The protein
CC of the invention is a human brain specific potassium channel protein. The
CC protein is used to treat and investigate disorders of the central nervous
CC system such as dementia and cerebral ischaemic sclerosis.
XX
SQ Sequence 3715 BP; 735 A; 1167 C; 1090 G; 723 T; 0 other;
Query Match 31.9%; Score 2664.8; DB 20; Length 3715;
Best Local Similarity 89.0%; Prod. No. 0;
Matches 2905; Conservative 0; Mismatches 347; Indels 12; Gaps 2;
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QY 61 CGCTTCGACGGCCACGACAGTAACCTTCGTGCTGGCAACGCCAGCTGGCGGGGCTCTTC 120
Db 216 CGCTTCGACGGGACGACAGTAACCTTCGTGCTGGCAACGCCAGCTGGCAGGGCTCTTC 275
QY 121 CCGCTGGTCTACTGCTCTGATGGCTTCCTGACCTCAGCGGCTTCCTCCGGGCTGAGGTC 180
Db 276 CCGTGGTCTACTGCTCCGATGGCTTCGTGACCTCAGCGGTTCTCCAGAGCTGAGGTC 335
QY 181 ATGACGGGGCTGTGCTCTGCTCTCTCTTTATGGCCAGACACCATGAGCTGCTCCCG 240
Db 336 ATGACGGAGGCTGTGCTCTGCTCTCTCTTCCTATGGCCAGACACCATGAGTTGGTCCG 395
QY 241 CAACAGATCCGCAAGGCTCGACGACACAGAGTTCAAGGCTGAGCTGATCTCTGAC 300
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QY 301 CGGAAGAGCGGCTCCCGTCTCTGGTGTCTCTCTGGATGTATACCATAAAGAAATGAGAAA 360
Db 456 CGGAAGAGCGGCTCCCATCTCTGGTGTCTCTCTGGATGTATACCTA*AAAAACGAGAG 515
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Db 2676 AAGTCTCTTTCCGGTGGGTCAAGTGTGCCAGAAATGTAGCAGAGCCCTCCCCAGGA 2735
QY 2572 CCAGAGAGCGCTGTCTACTGTTCCCATGGGCCAGAGGCAAGCAACACACACACA 2632
Db 2736 ACAGAGAGTGGCTGTCTACTGTCCTGTTGGCCAGTGTAGGCAAGAAACACACACA 2795
QY 2632 CTGACAAAGCTTCGGCAGGCGGTGACAGAGCTGTCTACACAGTGTCTGAGATGGGAA 2691
Db 2796 CTGACAAAGCTACGGCAGGCGGTGACGAGCTGTCTACACAGTGTCTGAGATGGCAG 2855
QY 2692 GGACTGCAGTCACTTCGCCAGGCTGTGCAGCTGTCTGGGCCACACAGGAGGTCCG 2751
Db 2856 GGACTGCAGTCACTTCGCCAGGCTGTGCAGCTGTCTGGGCCACACAGGAGGTCCG 2915
QY 2752 TGCCCTCGGCATCGGAGAGGCGGTGCCAGCAGCAGCTCCGGGCTGTCTGAGCT 2811
Db 2916 TGCCCGGGTATCAGAGAGGGGCTATGCCAGCAGCTGCCCTGCGGTCTCTA-AACCC 2975
QY 2812 CTGTGTGTGGACACTGGGCTATCTCTACTGCTGCAGCCCGCAGCTGGCTGTCTGTG 2871
Db 2976 CTGGTGTGACACTGGGCTATCTCTACTGCTGCAGCCCGCAGCTGGCTGTCTGTG 3035
QY 2872 AGTGGACTTGGCCCAACCTCGTCCGGGGCT---CCTCCCTCATGGCACCTGGGCC 2928
Db 3036 AGTGGACCTGGCTCAGCCCGCTCCAGGGCATCCCTCCCTCATGGCACCTGGGCC 3095
QY 2929 TGGGTGCCCGAGCTTCAGAGCTCCCTGGCTGGCCAGCAGCTTTGTGACCTCC 2986
Db 3096 TGGGGCCCCCAGCATCTCAGAGCTCCCTGGCTTCAGCCCGCAGCAGCTTTATGGACC 3155
QY 2989 ACCTCAGACTCAGAGCCCTCGCTCAGGAGACTCTGCTGTGAGCCAGCAGCTGCC 3042
Db 3156 ACCTCAGACTCAGAGCCCTGGCTGTGAGACTCTGCTGTGAGCCAGCAGCTGCC 3215
QY 3049 TCCCTCTCTCTAGGAAGGGGTAGGACTTGGCCCGGAGAGCTGTGAGCCAGCT 3108
Db 3216 TCACCCCTCTCTAGGAAGGGGTAGGACTTGGACTTGGACTTGGACTTGGACT 3275
QY 3109 GAGCTACAGACTTGAGAGCCCGCAGCAGGCTCAGGAGCTCTGCTGTGAGCCAGC 3162
Db 3276 GAGCTACAGACTTGAGAGCCCGCAGCAGGCTCAGGAGCTCTGCTGTGAGCCAG 3235
QY 3169 CCCACAGCTGGAGTGTGCTATTGGCTGCCATGGCTTGGCAGCTTCCAGTGGACC 3228
Db 3336 CCCACAGCTAGAGTGTGCTATCGGCTGCCATGGCTGCCATGGCTGCCATGGACC 3395
QY 3229 CAGGAAGAGGACAGGGGTCTGA 3252
Db 3396 CAGGAGGAGGACAGGAGTCTGA 3419

RESULT 8

AAx84911

ID AAx84911 standard; DNA: 3064 BP.

XX AAx84911:

AC AAx84911:

DT 28-SEP-1999 (first entry)

XX Human brain specific potassium channel protein coding sequence.

XX Brain specific potassium channel; human; central nervous system disorder;
XX dementia; cerebral ischaemic sclerosis; therapy: ss.
XX Homo sapiens.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 4..3057

FT /*tag= a

XX W09937677-A1.

XX

XX

XX

XX

PD 29-JUL-1999.
XX
PF 20-JAN-1999; 99WO-JP00190.
XX
PR 04-DEC-1998; 98JP-0346198.
XX
PR 23-JAN-1998; 98JP-0011434.
XX
PA (YAMA) YAMAMOUCHI PHARM CO LTD.
XX
XX Miyake A, Mochizuki S, Yokoi H;
XX WPI: 1999-458683/38.
DR P-PSDB: AAY22427.
DR
XX Potassium channel protein expressed specifically in brain tissue and
XX method for its production
XX
XX Claim 6; Page 44-49; 63pp; English.
XX
XX This sequence encodes the potassium channel protein of the invention,
XX that is expressed specifically in brain tissue. The protein is used to
XX treat and investigate disorders of the central nervous system such as
XX dementia and cerebral ischaemic sclerosis.
XX
XX Sequence 3064 BP; 554 A; 1042 C; 848 G; 620 T; 0 other;
XX
XX Query Match. 27.2%; Score 884.8; DB 20; Length 3064;
XX Best local Similarity 65.5%; Pred. No. 1.3e-151;
XX Matches 1408; Conservative 0; Mismatches 622; Indels 120; Gaps 3;
QY 1 ATCCGGCCATCGGGGCTCTCCCTGGCCCTCAGAACACCTTCCTGGACACCATCGCTAGG 60
Db 4 ATCCGGTCTATGAGGGGTGTGTCGCCCGCAAAACACCTTCCTGGACACCATCGCTAGG 63
QY 61 CGGTTCGACGGCAGCAGTAACTTCGTCTGGCAGCAGCCAGGTGSCGGGCTCTTC 120
Db 64 CGTTTCAACGAAACGACAGCAACTTCTCTGGTGGCCAGCCAGGACACGCGGCTT 123
QY 121 CCGTGTCTACTGCTGTGATGGCTTCTGTGACCTCAGGGCTTCTCCGGGCTGAGTTC 180
Db 124 CCATGCTGTACTGCTCGGAGGCTTCTGAGGCTCAGAGCTAGGGTGGACACGAGTTC 183
QY 181 ATCAGGGGGCTGTCCTCTCTCTTCCTTTATGGCCAGACACAGTGTCTCCGCTCCGC 240
Db 184 ATCAGAGAGCTGTGAGTGTCTCTCTAGGCTTCTAGGCTCAGAGCTGAGCTGAGCTG 243
QY 241 CAACAGATCCGAGGCGCTGGAGAGCAGAGAGTTCAGGCTGAGTGAICTGTATAC 300
Db 244 CAGGCTCTGCAAAAGCCCTTGGAGGGCCAGGAGCCGCGGCTGAAATCTGCTCTAC 303
QY 301 CGGAAGAGCGGCTCCGCT 360
Db 304 CGCAAGATGGCTCAGCTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 363
QY 361 GGGGAGTGGCT 414
Db 364 GGGGAGTGGCT 423
QY 415 CGAGGGGGCCCGCAGACAGATGGAAGGAGACAGGTGTGGCCGCGGCTATATGCGCGCA 474
Db 424 CTGGGCCCCCAGAGGCGCGGGGACATGATACAGAAATCTCTTGGTAGAAGGGA 483
QY 475 CGATCCAAAGGCTTCAATGCCAACCGCGCGGAGCGCGGCTCTCTCTCTCTCTCTCTCT 534
Db 484 GCCACCTGGAATTTCCGGTCTGCCAAGACGAGCGGTACTGTCTCTACACGCTGAGTACC 543
QY 535 GGGCAGCTGCAGAGAGCCCAAGGAGGAGCAGACAGCTCAATAGGGGTGTCTTGGGAG 594
Db 544 GGGCAGCTTGGCGCGGGGCGCCAGGAGGAGCATGAAGGCAATATAAGCTGTGTGAGCA 603
QY 595 AAACCAACTTGTCTGAGTACAAAGTAGCCGCTATCCGAGCTCCGCTCTCTCTCTCTCT 654
Db 604 AAGCCATCACTGCCGAGTACAAAGTGGCTCTCGGTGGGGGGTCTCGCTGCTCTCTCTCT 663

QY	655	CACGTGGGCACTGAGAGCAACCTGGGATGGCTTCATCCCTGCTGGCCACACACTGATGTG	714	1735	CAGCTSCACACTGTTTGAAGCGGCGCAGCGCGGCTGCTGGCGCACTGTCCTGGCCCTG	1794
DB	664	CATACAGCGTCTCCAAAGCCATCTGGGAGCGCTTAICCTCCCTGGCCACCTTGTACTGT	723	1795	CGGCGCGGCTCTCTGACGCGCGGCGGAGTACTCATCCACCAAGCGGATGCCCTGACGGC	1854
QY	715	GCTGTACTGTGCGCTACAGCGGTGTGTGAGCAGCAGCAGCGGCGGCGGCGGCGG	774	1720	AAGACTCGTGTCTGCGCTCCGCGGAGTACTGTGTGGCGGTGGGATSCCTGCGAGCA	1779
DB	724	GCGTCAACCTCCCTACAAAGTCTGTTCTCGGGTGACGATGACACCCCATCACCTGG	783	1855	CTCTACTGTGCTGCTGCTGCTCAAGAGGTGCTCAAGGTGCTGCTGCTGCTGCTGCTG	1914
QY	775	GGCGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	834	1780	CATTACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1839
DB	784	CGACACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	843	1915	CTAGGAGAGGCGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1962
QY	835	AATTCGGTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	894	1840	CTGGGAGAGGCGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1899
DB	844	AATTCGGGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	903	1963	GTGCTAAAGCGGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2004
QY	895	TGCTCCACTACCTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	954	1900	GGAGCAGACCCAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1959
DB	904	GGCTCCACTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	963	2005	GTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2064
QY	955	CTGCTACATGCTTCAAGTCAAGTGTACTTCTGCGGCGGCTGCTGCTGCTGCTGCTG	1014	1960	GGCTTCCAGCAGCTGAGCAGCGGCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2019
DB	964	CTGCTTACATCTCAACAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1023	2065	GCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2114
QY	1015	CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1074	2020	GGGGTGTGCTTCCGGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2069
DB	1024	CTGTTGCGGTGCTGCGGCTGCTGCGAGAGTGGAGCGTACTCTGCTGCTGCTGCTG	1083	RESULT 9		
QY	1075	GTGCTGACTGCTATGCGCGGTTTGGCGCTGCTGCGGCACTGCTGCTGCTGCTGCTG	1134	AA84918		
DB	1084	GTGCTGACTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1143	ID	AA84918	standard; DNA: 3736 BP.
QY	1135	TTTACATTTGCGAGCGGAGATCGAGCGAGCGATCCGAGCTGCCTGAGATGCTGCTG	1194	XX	AA84918;	
DB	1144	TATGCTATGCGCGCGGAGATGGAGCGCAATGATCCCGCTGCTGCTGCTGCTGCTG	1203	XX	20-SEP-1999	(first entry)
QY	1195	CTGAGGAGTGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1254	XX	Rat brain specific potassium channel protein coding sequence.	
DB	1204	TTCATGAGTGGGAGCGCTGAGAGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1259	XX	Brain specific potassium channel; central nervous system disorder;	
QY	1255	GGAGGAGAGCTCGCGGCGAGTGCACACTGCGAGCAGCAGCGAGCGGCGGAGCG	1314	XX	dementia; cerebral ischaemic sclerosis; therapy; probe; ss.	
DB	1251	-----	1250	XX	Rattus sp.	
QY	1315	GGGTGAGTGTGGCGGCGGCTGCTGCGAGCGCTATGCTGCTGCTGCTGCTGCTGCTG	1374	XX	WO9937677-A1.	
DB	1251	-----GTTGGCGCGCCATCAGCGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1299	XX	29-JUL-1999.	
QY	1375	GCATCAGGCGCTCAGCAGCGTGGCTTGGCGAGCTGTCGGCGAGCGTTCGGCGAGC	1434	XX	20-JAN-1999; 99WO-JP00190.	
DB	1300	ACTTAAGAGCGCTCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1359	XX	04-DEC-1998; 98JP-0346198.	
QY	1435	AAGATCTCTCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1494	XX	23-JAN-1996; 98JP-0011434.	
DB	1360	ANGATCTCTCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1419	XX	(YAMA) YAMANOUCHI PHARM CO LTD.	
QY	1495	AAGCTGAGCGGCTCAGCAGCGTGGCTTGGCGAGCTGTCGGCGAGCTGTCGGCGAG	1554	XX	Miyake A, Mochizuki S, Yokoi H;	
DB	1420	AAGCTGAGCGGCTCAGCAGCGTGGCTTGGCGAGCTGTCGGCGAGCTGTCGGCGAG	1479	XX	WPI; 1999-458683/38.	
QY	1555	CGGAGCTGCGGCTACATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1614	XX	Potassium channel protein expressed specifically in brain tissue and	
DB	1480	AAGGACCTCAAGGACTTCACTCGTGTGCAACCGCTGCTGCTGCTGCTGCTGCTGCTG	1539	XX	method for its production	
QY	1615	CTGGAGTACTTCCAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1674	XX	Example 3; Page 57-59; 63pp; English.	
DB	1540	CTGGAATCTTCCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1599	XX	This sequence encodes a rat potassium channel protein, and was used as a	
QY	1675	CAGAGCTCTCCCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1734	XX	probe to isolate DNA encoding the protein of the invention. The protein	
DB	1600	CGTGAATCTCCAGAGAGCTGAGAGCTGACATGCTATGCACTGAACTGGGAGATCTG	1659	XX	of the invention is a human brain specific potassium channel protein. The	
				XX	protein is used to treat and investigate disorders of the central nervous	
				XX	system such as dementia and cerebral ischaemic sclerosis.	
				XX	Sequence 3736 BP; 706 A; 1210 C; 1000 G; 820 T; 0 other;	
				XX	Query Match 26.7%; Score 869.8; DB 20; Length 3736;	

RESULT 10
 AA250454
 ID AA250454 standard; cDNA: 1132 BP.
 XX
 AC AA250454:
 XX
 DT 18-MAY-2000 (first entry)
 XX
 DE Human potassium channel; molecule ERG-LP1; partial cDNA.
 XX
 KW Human; potassium channel molecule: ERG-like protein 1; partial ERG-LP1;
 KW neuroprotective; antiParkinsonian; anticonvulsant; antidepressant;
 KW neuroleptic; nootropic; treatment; CNS disorder; central nervous system;
 KW potassium channel mediated disorder; epilepsy; Alzheimer's disease;
 KW Parkinson's; multiple sclerosis; depression; schizophrenia; amnesia;
 KW chromosome 12q11-13; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 5'UTR 1..262
 FT mat_peptide 263..1132
 FT /*tag= a
 FT /*tag= b
 FT /product= "Partial ERG-LP1"
 FT /trans_except= (pos:1031..1033, aa:Arg)
 FT /note= "This region is specifically claimed"
 XX
 PN WO200005346-A1.
 XX
 PD 03-FEB-2000.
 XX
 PD 2i-JUL-1999; 99WO-US16752.
 XX
 PD 21-JUL-1998; 98US-0119855.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PA Curtis RAJ;
 XX
 PI WPI: 2000-182682/16.
 XX
 DR P-PSDB; AA44906.
 XX
 PT Novel gene encoding potassium channel molecule useful in treating
 PT central nervous system disorders such as Alzheimer's disease, multiple
 PT sclerosis, and schizophrenia.
 XX
 PS Claim 2; Fig 5; 144pp; English.
 XX
 CC The present sequence is a cDNA encoding partial ERG-like protein 1
 CC (ERG-LP1) which is a member of ERG potassium channel family. This
 CC sequence is derived from a human EST (expressed sequence tag)
 CC IMAGE clone 37299. ERG-LP1 is expressed exclusively in the brain.
 CC Highest expression is found in cortical regions, hippocampus, caudate
 CC and amygdala. ERG-LP1 gene was mapped to human chromosome 12q11-13,
 CC between markers W1-7107 and W1-6327.
 CC The protein functions as a potassium channel modulator and
 CC has neuroprotective, antiParkinsonian, anticonvulsant, antidepressant,
 CC neuroleptic and nootropic activities. The present sequence is
 CC useful for treating several potassium channel mediated disorders (CNS
 CC disorders) such as Alzheimer's disease, Parkinson's disease, multiple
 CC sclerosis, epilepsy, depression, schizophrenia disorders and amnesia.
 XX
 SQ Sequence 1132 BP; 189 A; 376 C; 379 G; 188 T; 0 other;
 XX
 Query Match 26.0%; Score 844.4; DB 21; Length 1132;
 Best Local Similarity 99.9%; Pred. No. 2.5e-144;
 Matches 845; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 ATGCGCGCATGCGGGGCTCTCTGGCGCGCAGAAACCTTCTCTGGACACCATCGCTACG 50
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 263 ATGCGCGCATGCGGGGCTCTCTGGCGCGCAGAAACCTTCTCTGGACACCATCGCTACG 322
 QY 61 CGCTTCGACGGCAGCCACAGTAACCTCGTGTGGGCAAGCCGCGGAGTGGCGGGCTCTTC 120
 DB 323 CGCTTCGACGGCAGCCACAGTAACCTCGTGTGGGCAAGCCGCGGAGTGGCGGGCTCTTC 382
 QY 121 CCGGTGGTCTACTGCTGTGATGGGTTCCTGTGACCTCAGCGGCTTCTCCCGGGGTGAGGTC 180
 DB 383 CCGGTGGTCTACTGCTGTGATGGGTTCCTGTGACCTCAGCGGCTTCTCCCGGGGTGAGGTC 442
 QY 181 ATGCGCGGGGCTGTGCTGTCT 240
 DB 443 ATGCGCGGGGCTGTGCTGTCT 502
 QY 241 CAACAGATCCGCAAGGCCCTTGAGCAGCAGCAGAGGAGTTCAGAGCTGAGCTGATCCGTGATC 300
 DB 503 CAACAGATCCGCAAGGCCCTTGAGCAGCAGCAGAGGAGTTCAGAGCTGAGCTGATCCGTGATC 562
 QY 301 CGGAGAGCGGGCTCGGCTCTGTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
 DB 563 CGGAGAGCGGGCTCGGCTCTGTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 622
 QY 361 GGGGAGGTGGCT 420
 DB 623 GGGGAGGTGGCT 682
 QY 421 GGGCGCGCAGATGGAAGGAGCAGAGTGGTGGCGGGCGCGCGGTGTGTGTGTGTGTGTGTGT 480
 DB 683 GGGCGCGCAGATGGAAGGAGCAGAGTGGTGGCGGGCGCGCGGTGTGTGTGTGTGTGTGTGT 742
 QY 481 AAGGCTTCAATGCGCAAGCGCGGCGGAGCGCGGCGGTGTGTGTGTGTGTGTGTGTGTGTGT 540
 DB 743 AAGGCTTCAATGCGCAAGCGCGGCGGAGCGCGGCGGTGTGTGTGTGTGTGTGTGTGTGTGT 802
 QY 541 CTGCAGACAGCCCAAGGGCAGCAGCAGCTCANTAGGGGGTGTGTGGGAGAAACCA 600
 DB 803 CTGCAGACAGCCCAAGGGCAGCAGCAGCTCANTAGGGGGTGTGTGGGAGAAACCA 862
 QY 601 AACTTGCCTGAGTACAAAGTAGCCGCTATCCGGAAGTCCGCTTTCATCCTCTTSCACTGT 660
 DB 863 AACTTGCCTGAGTACAAAGTAGCCGCTATCCGGAAGTCCGCTTTCATCCTCTTSCACTGT 922
 QY 661 GGGGCACTGAGAGCCACCTGGGATGGCTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
 DB 923 GGGGCACTGAGAGCCACCTGGGATGGCTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 982
 QY 721 ACTGTGCCCTACAGCGTGTGTGTGAGCAGCAGCAGGAGCCAGTGGCGCGCGCGCGCGCG 780
 DB 983 ACTGTGCCCTACAGCGTGTGTGTGAGCAGCAGCAGGAGCCAGTGGCGCGCGCGCGCGCG 1042
 QY 781 CCAGCGCTGTGACCTGGCGCTGGAGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
 DB 1043 CCAGCGCTGTGACCTGGCGCTGGAGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
 QY 841 CGTACC 846
 DB 1103 CGTACC 1106
 RESULT 11
 AA293334
 ID AA293334 standard; cDNA: 3742 BP.
 XX
 AC AA293334:
 XX
 DT 04-JUL-2000 (first entry)
 XX
 DE Rat elk1 potassium channel gene.
 XX
 KW Elk1; elk2; eag1; eag2; erg1; potassium channel; membrane protein;
 KW drug screening; hypertension; renal failure; diabetes insipidus;
 KW diabetic nephropathy; hypothyroidism; goiter; hypoparathyroidism;
 KW pancreatic insufficiency; diabetes mellitus; cystic fibrosis;

Db 1181 ATTGAAAATGAGAGGAGGAGACACAGCCTTCTCAAGTGGGAAGTCGGTTGGCTTCAC 1240
 QY 1201 GAGTGGCCGCGGAGTCCCTACTACTACTGCTGGTGGCCGAGGCCAGCTGGAGG 1260
 Db 1241 GAGTGGGAAGAGACTGGAATCTCCGTACTAC----- 1273
 QY 1261 AACAGCTCCGGCAGAGTGACAACTGTCAGCAGCAGCAGGAGGCCAACGGAGGGGCTG 1320
 Db 1274 -----GGGAAC 1279
 QY 1321 GAGTGTGCTGGGCGCGCTGGCAGCGCTACATCACTCCCTACTGCGACTC 1380
 Db 1280 AACAGCTGGGCGCGCTGGCAGCGCTATATCGCAGCTTGTACTTCACTCTC 1339
 QY 1381 AGAGCCTCAGCAGGTGGCTGGCAGCGTTCGCGCAACGTGCGCAACAGCGACCGAGAGATC 1440
 Db 1340 AGCAGCCTCAGCAGGTGGGATTTGGGATGTGCGCTAACAGCGATGCAAGAGATC 1399
 QY 1441 TTCTCCATCTGCACCATCTCACTGCGCGCTGATGACGCGGTGGTGTGGGAAGTG 1500
 Db 1400 TTCTCCATCTGACCATGTGATGAGCGCTGATGATGCTTGGTATTTGGGAATGTG 1459
 QY 1501 AGGCGCATCATCAGCGCATGTACGCGCGCGCTTCTGTACACAGCGCGCATGCTGAG 1560
 Db 1460 ACTGCCATCATACAGAGATGTACTCTAGATGGAGCCTGTACCATACTAGAACAGGAC 1519
 QY 1561 CTGGCGGACTACATCGCATCCACCGTATCCCGAGCGCTCAAGCAGCGCATGCTGAG 1520
 Db 1520 CTAAAGAGCTTATCGGTGTGATCCTGCGCGAGCACTCAAGCAGAGATGCTGAG 1579
 QY 1621 TACTTCAGCGCAGCTGGCGGTGAACAAATGGCATCGACACCGCGAGCTGCTCAGAGC 1630
 Db 1580 TACTTTACAGCAACTGTGCTGTCAACAATGATAGATTCATATGAGCTTTGAGAGAC 1639
 QY 1681 CTCCCTGAGAGCTGGCGGACACATCGCATGCGCATGCGCATGCGCATGCGCATGCG 1740
 Db 1640 TTCCAGATGAGTGGCTGTGACATCAATGCAATGCAATGCAATGCAATGCAATGCA 1699
 QY 1741 CCAGCTTTTGGCGGCGGAGCGCGCTGCTGCGGCGCTGCTGCGGCGCTGCGGCG 1800
 Db 1700 TCCTGTTTGAATGTGTAGCGGCGCTGCTGCGGCGCTGCTGCTGCTGCTGCTGCTG 1759
 QY 1801 GCCTTCGACGCGCGGAGTACCTCATCCACAGCGGATGCGCGCTGCGGCGCTGCTG 1860
 Db 1760 TCAITCTGTCGCGGAGGAGTATCTGCTGCGCGGAGGATGCTGCGGCGGAGGATGCT 1819
 QY 1861 TTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
 Db 1820 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1879
 QY 1921 AAGGCGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
 Db 1880 AAGGCGGATTTAATGGAGCAATTTATCAATTAAGACCAAGTGTATCAAGCAAGCT 1939
 QY 1981 GAGCTGAAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
 Db 1940 GAGCTGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1999
 QY 2041 AGCCTTGGCTGTACCGGAGTTTGGCGCGGCTTCACTGCTGCGGCTCCGAGGCGAGCTC 2100
 Db 2000 GTGCTGGGCTTTAGCGAGTACGACACAAATTC-GTAGAAGACATCCGACGAGCTC 2058
 QY 2101 AGCTAACCTGGGCTGG 2120
 Db 2059 ACATACAGCTTCGAGAAG 2078

RESULT 12
 AA250455
 ID AA250455 standard: cDNA: 5107 BP.
 XX
 AC AA250455:

XX DT 16-MAY-2000 (first entry)
 DE Human potassium channel molecule ERG-LP2 full-length cDNA.
 XX KW Human: potassium channel molecule; ERG-like protein 2; ERG-LP2;
 KW neuroprotective; antiParkinsonian; anticonvulsant; antidepressant;
 KW neuroleptic; nootropic; treatment; CNS disorder; central nervous system;
 KW potassium channel mediated disorder; epilepsy; Alzheimer's disease;
 KW Parkinson's; multiple sclerosis; depression; schizophrenia; amnesia;
 KW chromosome 3p21.3-24.3; ss.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 DE 5'UTR 1..195
 FT /*tag= a
 FT CDS 196..3519
 FT /*tag= b
 FT /*product= "ERG-LP2"
 FT 3'UTR 3520..5107
 FT /*tag= c
 XX PN WC200005346-A1.
 XX PD 03-FEB-2000.
 XX PF 21-JUL-1999; 99WO-US16752.
 XX PR 21-JUL-1998; 98US-0119855.
 XX PA (MILL-) MILLENNIUM PHARM INC.
 XX PJ Curtis RAJ;
 XX DR WPI: 2000-182682/16.
 XX P-PSDB: AAY44907.
 PT Novel gene encoding potassium channel molecule useful in treating
 PT central nervous system disorders such as Alzheimer's disease, multiple
 PT sclerosis, and schizophrenia
 XX Example 1: Fig 8; 144pp; English.
 XX The present sequence is a cDNA encoding full-length ERG-like protein 2
 CC (ERG-LP2) which is a member of ERG potassium channel family. This
 CC sequence is a result of additional sequencing of clone ilhbaa042h05 which
 CC was obtained from human brain library. ERG-LP2 gene is mapped to
 CC human chromosome 3p21.3-24.3, between markers WI-4218 and RP-L15_1. It
 CC is predominantly expressed in the brain.
 CC The protein functions as a potassium channel modulator and
 CC has neuroprotective, antiParkinsonian, anticonvulsant, antidepressant,
 CC neuroleptic and nootropic activities. The present sequence is
 CC useful for treating several potassium channel mediated disorders (CNS
 CC disorders) such as Alzheimer's disease, Parkinson's disease, multiple
 CC sclerosis, epilepsy, depression, schizophrenic disorders and amnesia.
 XX Sequence 5107 BP; 1486 A; 1137 C; 1092 G; 1391 T; 1 other;

Query Match 23.4%; Score 761.2; DB 21; Length 5107;
 Best Local Similarity 62.2%; Pred. No. 3.8e-129;
 Matches 1319; Conservative 0; Mismatches 708; Indels 93; Gaps 4;
 QY 1 ATGCGGGCCATCGGGGCTCTCTGCGGCTCAGAACACCTTCTGTCAGACACCTTCGCTAGC 60
 Db 196 ATGCGGGTTATGAAGAGATTACTGGCGCGCAAAACACCTTCTGTCAGACACCTTCGCGCAC 255
 QY 61 CGCTTCGAGCGGACGACAGTAACTTCTGCTGGCAACGCCAGCTGGCGGCTCTTC 120
 Db 256 CGTTTIGAGGACACATAGCACTTCTGTCGCAATGCCAGCTGAGGCTTC 315
 QY 121 CCCGTGGTCTACTGCTGTGATGGCTTCGTGACCTCAGGGCTTCCTCCCGGGCTAGGTC 180

KW	immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;	PR	14-SEP-2000; 2000US-0233064.
KW	antiparkinsonian; antispasmodic; antianemic; antiarthritic; cancer;	PR	14-SEP-2000; 2000US-0233065.
KW	antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;	PR	21-SEP-2000; 2000US-0234223.
KW	antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;	PR	21-SEP-2000; 2000US-0234274.
KW	antiparasitic; cardiac; immune disorder; cardiovascular disorder;	PR	25-SEP-2000; 2000US-0234997.
KW	neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.	PR	25-SEP-2000; 2000US-0234998.
XX		PR	26-SEP-2000; 2000US-0235484.
OS	Homo sapiens.	PR	27-SEP-2000; 2000US-0235814.
XX		PR	27-SEP-2000; 2000US-0235836.
PN	WO200159063-A2.	PR	29-SEP-2000; 2000US-0236327.
XX		PR	29-SEP-2000; 2000US-0236367.
PD	16-AUG-2001.	PR	29-SEP-2000; 2000US-0236368.
XX		PR	29-SEP-2000; 2000US-0236369.
XX		PR	29-SEP-2000; 2000US-0236370.
PF	17-JAN-2001; 2001WO-US01334.	PR	02-OCT-2000; 2000US-0236802.
XX		PR	02-OCT-2000; 2000US-0237037.
PR	31-JAN-2000; 2000US-0179065.	PR	02-OCT-2000; 2000US-0237038.
PR	04-FEB-2000; 2000US-0180628.	PR	02-OCT-2000; 2000US-0237039.
PR	24-FEB-2000; 2000US-0184864.	PR	02-OCT-2000; 2000US-0237040.
PR	02-MAR-2000; 2000US-0186350.	PR	13-OCT-2000; 2000US-0239935.
PR	16-MAR-2000; 2000US-0189874.	PR	13-OCT-2000; 2000US-0239937.
PR	17-MAR-2000; 2000US-0190076.	PR	20-OCT-2000; 2000US-0240560.
PR	18-APR-2000; 2000US-0198123.	PR	20-OCT-2000; 2000US-0241785.
PR	19-MAY-2000; 2000US-0205515.	PR	20-OCT-2000; 2000US-0241786.
PR	07-JUN-2000; 2000US-0209467.	PR	20-OCT-2000; 2000US-0241787.
PR	28-JUN-2000; 2000US-0214886.	PR	20-OCT-2000; 2000US-0241808.
PR	30-JUN-2000; 2000US-0215135.	PR	20-OCT-2000; 2000US-0241809.
PR	07-JUL-2000; 2000US-0216647.	PR	20-OCT-2000; 2000US-0241826.
PR	07-JUL-2000; 2000US-0216880.	PR	20-OCT-2000; 2000US-0242221.
PR	11-JUL-2000; 2000US-0217487.	PR	01-NOV-2000; 2000US-0244617.
PR	11-JUL-2000; 2000US-0217496.	PR	01-NOV-2000; 2000US-0244617.
PR	14-JUL-2000; 2000US-0218290.	PR	08-NOV-2000; 2000US-0246474.
PR	25-JUL-2000; 2000US-0220953.	PR	08-NOV-2000; 2000US-0246475.
PR	26-JUL-2000; 2000US-0220954.	PR	08-NOV-2000; 2000US-0246476.
PR	14-AUG-2000; 2000US-0224518.	PR	08-NOV-2000; 2000US-0246477.
PR	14-AUG-2000; 2000US-0224519.	PR	08-NOV-2000; 2000US-0246478.
PR	14-AUG-2000; 2000US-0225213.	PR	08-NOV-2000; 2000US-0246523.
PR	14-AUG-2000; 2000US-0225214.	PR	08-NOV-2000; 2000US-0246524.
PR	14-AUG-2000; 2000US-0225266.	PR	08-NOV-2000; 2000US-0246525.
PR	14-AUG-2000; 2000US-0225267.	PR	08-NOV-2000; 2000US-0246526.
PR	14-AUG-2000; 2000US-0225268.	PR	08-NOV-2000; 2000US-0246527.
PR	14-AUG-2000; 2000US-0225270.	PR	08-NOV-2000; 2000US-0246528.
PR	14-AUG-2000; 2000US-0225447.	PR	08-NOV-2000; 2000US-0246532.
PR	14-AUG-2000; 2000US-0225457.	PR	08-NOV-2000; 2000US-0246609.
PR	14-AUG-2000; 2000US-0225758.	PR	08-NOV-2000; 2000US-0246610.
PR	14-AUG-2000; 2000US-0225759.	PR	08-NOV-2000; 2000US-0246611.
PR	18-AUG-2000; 2000US-0226279.	PR	08-NOV-2000; 2000US-0246613.
PR	22-AUG-2000; 2000US-0226681.	PR	17-NOV-2000; 2000US-0249207.
PR	22-AUG-2000; 2000US-0226865.	PR	17-NOV-2000; 2000US-0249208.
PR	22-AUG-2000; 2000US-0227182.	PR	17-NOV-2000; 2000US-0249209.
PR	23-AUG-2000; 2000US-0227009.	PR	17-NOV-2000; 2000US-0249210.
PR	30-AUG-2000; 2000US-0228924.	PR	17-NOV-2000; 2000US-0249211.
PR	01-SEP-2000; 2000US-0229287.	PR	17-NOV-2000; 2000US-0249212.
PR	01-SEP-2000; 2000US-0229343.	PR	17-NOV-2000; 2000US-0249213.
PR	01-SEP-2000; 2000US-0229344.	PR	17-NOV-2000; 2000US-0249214.
PR	01-SEP-2000; 2000US-0229345.	PR	17-NOV-2000; 2000US-0249215.
PR	05-SEP-2000; 2000US-0229509.	PR	17-NOV-2000; 2000US-0249216.
PR	05-SEP-2000; 2000US-0229513.	PR	17-NOV-2000; 2000US-0249217.
PR	06-SEP-2000; 2000US-0230437.	PR	17-NOV-2000; 2000US-0249218.
PR	06-SEP-2000; 2000US-0230438.	PR	17-NOV-2000; 2000US-0249219.
PR	08-SEP-2000; 2000US-0231242.	PR	17-NOV-2000; 2000US-0249224.
PR	08-SEP-2000; 2000US-0231243.	PR	17-NOV-2000; 2000US-0249245.
PR	08-SEP-2000; 2000US-0231244.	PR	17-NOV-2000; 2000US-0249264.
PR	08-SEP-2000; 2000US-0231413.	PR	17-NOV-2000; 2000US-0249265.
PR	08-SEP-2000; 2000US-0231414.	PR	17-NOV-2000; 2000US-0249297.
PR	08-SEP-2000; 2000US-0232080.	PR	17-NOV-2000; 2000US-0249299.
PR	08-SEP-2000; 2000US-0232081.	PR	17-NOV-2000; 2000US-0249300.
PR	12-SEP-2000; 2000US-0231968.	PR	01-DEC-2000; 2000US-0250391.
PR	14-SEP-2000; 2000US-0232357.	PR	05-DEC-2000; 2000US-0251030.
PR	14-SEP-2000; 2000US-0232398.	PR	05-DEC-2000; 2000US-0251988.
PR	14-SEP-2000; 2000US-0232399.	PR	05-DEC-2000; 2000US-0256719.
PR	14-SEP-2000; 2000US-0232400.	PR	08-DEC-2000; 2000US-0251479.
PR	14-SEP-2000; 2000US-0232401.	PR	08-DEC-2000; 2000US-0251856.
PR	14-SEP-2000; 2000US-0233063.	PR	08-DEC-2000; 2000US-0251868.

PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254057.
 PR 05-JAN-2001; 2001US-0259678.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-541565/60.
 XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating nervous system
 PT cancers and metastases -
 XX
 PS Disclosure; SEQ ID NO 12345; 1701pp + Sequence Listing; English.
 XX
 CC The invention relates to novel genes (ABA:1004-ABA21534) and proteins
 CC (ABR14678-ABR18001) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
 XX
 SQ Sequence 10579 BP; 2298 A; 2894 C; 3129 G; 2256 T; 0 other;
 Query Match 18.5%; Score 501; DB 22; Length 10579;
 Best Local Similarity 100.0%; Pred. No. 5.2e-100;
 Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 XX AAK70045;
 AC AAK70045;
 DT 06-NOV-2001 (first entry)
 XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24857.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24857.
 KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytostatic; gene therapy; vaccine; metastasis; ds.
 OS Homo sapiens.
 XX WO200157182-A2.
 PN 09-AUG-2001.
 PD 17-JAN-2001; 2001WO-US01354.
 PF 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
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 PR 19-MAR-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
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 PR 30-JUN-2000; 2000US-0215135.
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 PR 14-JUL-2000; 2000US-0217496.
 PR 26-JUL-2000; 2000US-0220363.
 PR 26-JUL-2000; 2000US-0220364.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225271.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
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 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226868.
 PR 23-AUG-2000; 2000US-0227182.
 PR 30-AUG-2000; 2000US-0227009.
 PR 01-SEP-2000; 2000US-0229287.

PR 20-OCT-2000; 2000US-0241826.
 PR 20-OCT-2000; 2000US-0242221.
 PR 01-NOV-2000; 2000US-024617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
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 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
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 PR 17-NOV-2000; 2000US-0249207.
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 PR 17-NOV-2000; 2000US-0249244.
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 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250391.
 PR 01-DEC-2000; 2000US-0251160.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
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 PR 05-JAN-2001; 2001US-0259678.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-541565/60.
 XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating nervous system
 PT cancers and metastases -
 XX
 PS Disclosure; SEQ ID NO 12346; 1701pp - Sequence listing; English.
 XX
 CC The invention relates to novel genes (AB11004-ABA21534) and proteins
 CC (AB114678-AB18001) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune

CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral ataxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIFO at ftp.wifo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 28995 BP; 6151 A; 8327 C; 8051 G; 6466 T; 0 other;

Query Match 18.5%; Score 601; DB 22; Length 28995;
 Best Local Similarity 100.0%; Pred. No. 5.9e-100;
 Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Search completed: October 1, 2003, 16:22:13
 Job time : 810 secs

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RESULT 2
US-09-343-494-2
; Sequence 2, Application US/09343494
; Patent No. 6413741
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy J.
; APPLICANT: Wickenden, Alan
; APPLICANT: ICRgen, Incorporated
; TITLE OF INVENTION: Human Elk, a Voltage-Gated Potassium Channel Subunit
; FILE REFERENCE: 018512-001320US
; CURRENT APPLICATION NUMBER: US/09/343.494
; CURRENT FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: US 60/091.469
; EARLIER FILING DATE: 1998-07-01
; EARLIER APPLICATION NUMBER: US 60/116.621
; EARLIER FILING DATE: 1999-01-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2

; LENGTH: 3249
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3249)
; OTHER INFORMATION: hElk
US-09-343-494-2

Query Match 99.8%; Score 3245.8; DB 4; Length 3249;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3247; Conservative 0; Mismatches 2; Indels 0; Caps 0;

Qy 1 ATGCGCGGCATGCGGGGCTCTCTGGCGCTTCAGAACACTTCTTGACACCATCGCTACG 60
Db 1 ATGCGCGGCATGCGGGGCTCTCTGGCGCTTCAGAACACTTCTTGACACCATCGCTACG 60
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Db 61 CGCTTCGACGCGCAGCAGTAACTTCGTGCTGGCAACGCCAGGTGGGGGCTCTTC 120
Qy 121 CCCGTGTCTACTGCTCTGTATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC 180
Db 121 CCCGTGTCTACTGCTCTGTATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC 180
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 DB 3001 GAGCGCCCTGCTCAGGAGACTCTGCTCTGAGCGCCAGCAGCCCTGCTCCCTCCCTCCT 3060
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; LOCATION: {104}...{3352}
US-09-358-383C-1

Query Match									
Best Local Similarity 98.28; Pred. No. 0;									
Matches 3192; Conservative 0; Mismatches 60; Indels 0; Gaps 0;									
QY	1	ATGCCGCGCATGCGGGGCGCTCCCTGGCGGCTCAGAAACACCTTCCTGACACCATGCGCTAGC	60						
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QY	61	CGCTTCACGCGCAGCGACACTAACTTCGTGCTGGGCAACGCCACCGTGGCGGCGCTTC	120						
DB	164	CGCTTCACGCGCAGCGACACTAACTTCGTGCTGGGCAACGCCACCGTGGCGGCGCTTC	223						
QY	121	CCCGTGGTCTACTGCTCTGATGGCTTCGTGACCTCACGGGCTTCCTCCGGGCTGAGGTC	180						
DB	224	CCCGTGGTCTACTGCTCTGATGGCTTCGTGACCTCACGGGCTTCCTCCGGGCTGAGGTC	283						
QY	181	ATGCAGCGGGCTGTGCTGCTCTCTCCCTTTATGGGCCAGACACCTGAGCTCGCGG	240						
DB	284	ATGCAGCGGGCTGTGCTGCTCTCTCTTTATGGGCCAGACACCTGAGCTCGFCGCG	343						
QY	241	CAACAGATCCGCAAGGCCCTGGACGAGCACAAGGAGTTCAAGGCTGAGTGTCTGTATC	300						
DB	344	CAACAGATCCGCAAGGCCCTGGACGAGCACAAGGAGTTCAAGGCTGAGTGTCTGTATC	403						
QY	301	CGGAAGAGCGGGTCCCGTTCTGGTGTCTCTCTGATGTGATACCCATAAGATGAGAAA	360						
DB	404	CGGAAGAGCGGGTCCCGTTCTGGTGTCTCTCTGATGTGATACCCATAAGATGAGAAA	463						
QY	361	GGGAGGTGGCTCTCTTCCTAGTCTCTCAAGGACATACGCAAAACCAAGAACCGAGGG	420						
DB	464	GGGAGGTGGCTCTCTTCCTAGTCTCTCAAGGACATCAGTGAACCAAGAACCGAGGG	523						
QY	421	GGCCCGGACAGATGGAAGGAGACAGTGTGTGGCGGCGCGCAATGGCGGGCACGATCC	480						
DB	524	GGCCCTGCACAGATGGAAGGAGACAGTGTGTGGCGGCGCGCAATGGCGGGCACGATCC	583						
QY	481	AAAGGCTTCATGTGCAACCGGCGGAGCGGGCGGTGCTACACACCTGTCCGGGCGAC	540						
DB	584	AAAGGCTTCATGTGCAACCGGCGGAGCGGGCGGTGCTACACACCTGTCCGGGCGAC	643						
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DB	644	CTGCAGAGCAGCCCAAGGCGAAGCACAAGCTCAATAAGGGGGTGTGGGAGAAAGCCA	703						
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QY	661	GGGCACTGAGAGCCACCTGSGATGGCTTCATCTCTCGCCACACTCTATGTCGGTGT	720						
DB	764	GGGCGCTGAGGGCCACCTGSGATGGCTTCATCTCTCGCCACACTCTATGTCGGTGT	823						
QY	721	ACTGTGCGCTACAGGTGTGTGTGAGCAGCAGCGAGGCCAGTCCGCCCGCGCGCG	780						
DB	824	ACCGTGCGCTACAGCGTGTGTGTGAGCAGCAGCGAGGCCAGTCCGCCCGCGCGCCA	883						
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DB	944	CGTACCACTTGTGTCCAAAGTCGGGCGAGGTGTGTTCGCCCAAGTCCATTTGCCCT	1003						
QY	901	CACCTAGCTCACACCTGTCTCTGCTGGATGTCTATCGAGCGGTGCCCTTTGACCTGCTA	960						
DB	1004	CACCTAGCTCACACCTGTCTCTGCTGGATGTCTATCGAGCGGTGCCCTTTGACCTGCTG	1063						
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DB	1244	ATTGGTCAAGCGGAGATCGAGACGAGTCCGAGTCCGCTGAGATTCGCTGCTGCTGAG	1303
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QY	1261	AACAGCTCCGCGGAGAGTCAACTSCAGCAGCAGCAGGAGGCCAACGGGACGGGCTG	1320
DB	1364	AACAGCTCTGGCCAGAGTGAACACTGCAGCAGCAGCAGGAGGCCAACGGGAGGGCTG	1423
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DB	1424	GAGTGTGCGGCGGCTGCTGCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1483
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DB	1484	AGCAGCTCACCAGCGTGGCTTCGGCAAGCTTCGCGCAACGAGCAGCAGCAGCAGCAGC	1543
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DB	1784	CTCCTGACGAGTGCAGCAGCATGCCATGACCTGACACAGGAGGTGCTGCTGAGAGC	1843
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DB	1844	CACTGTGTTGAGGGCGGCGGCTGCTGCGGCACTGCTGCGGCTGCGGCGGCTGCGGCGG	1903
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DB	1904	GCTTCTGACCGCGGCGGAGTACCTCATCCACAGGCGATGCCCTGAGGCGGCTGCTAC	1963
QY	1861	TTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1920
DB	1964	TTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2023
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DB	2084	GATGTGAAGGCGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2143
QY	2041	AGCTTGGCTGTACCCCGGAGTTTGGCGCGGCTTCAAGTGTGCTGCTGCTGCTGCTGCTG	2100
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QY 3241 ACAGGGGTCTGA 3252
DB 3344 ACAGGGGTCTGA 3355

RESULT 5
US-09-358-383C-3
: Sequence 3, Application US/09358383C
: Patent No. 6518398
: GENERAL INFORMATION:
: APPLICANT: CURTIS, RORY A. J.
: TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
: FILE REFERENCE: MNI-055CP
: CURRENT APPLICATION NUMBER: US/09/358,383C
: PRIOR FILING DATE: 1999-07-21
: PRIOR APPLICATION NUMBER: USSN 09/119,855
: PRIOR FILING DATE: 1998-07-21
: NUMBER OF SEQ ID NOS: 36
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 3
: LENGTH: 3249
: TYPE: DNA
: ORGANISM: Macaca sp.
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(3249)
US-09-358-383C-3

Query Match 97.0%; Score 3153; DB 4; Length 3249;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 3189; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

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QY 301 CGAAGAGGGGCTCCCGTCTGCTGCTCTCTGATGTATGCCATAAAGAAATGAGAAA 360
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QY 361 GGGGAGTGGCTCTTCTTCTAGTCTCTCAAGGACATCAGCAACCAAGAACCGAGGG 420
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QY 421 GGCCCGACAGATGGAAGGAGACAGGTGGTGGCCGGGCGGATATGGCGGCGACGATCC 480
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DB 481 AAAGGCTTCAATCCCAACCGGGGAGGCGGCGGCTGTCTTACCACTGTGCGGGGAC 540
QY 541 CTGACAGAGAGCCCAAGGGCAAGCAAGCTCAATAAGGGGGTGTGTTGGGAGAAACA 600
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541 CTGCAAGAGCGCCCAAGGCAAGCACAAGCTCAATAAGGGGTGTTGGGAGAAGCCA 609
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QY CACTACGTACACACTGGTTCCTGCTGATGTCTATCGCAGCGTGGCCCTTTGACCTGCTG 960
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Db 2016 GCTCTCTACTTGTGTGTCTGAGTTCATGAGAGTGTCAAGGTGGCGACCGTGTGGCG 2075
QY 1912 ATCTAGGGAAGGCGAGCTGATCGGTGTGAGTGTGCGCGCGGAGCAGGTGGTAAAG 1971
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QY 1972 GCAATGCGAGTGAAGGGCTGAGTACTGCGTCTGAGTGTGCGAGTGTGCGAGTGTGCG 2031
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QY 2032 CTGCAAGCAGAGCTTGCCTGTACCGCGAGTTGCGCGCGGCTTCACTGCTGCGCTCGA 2091
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QY 3169 CCGCAGAGCTGAGAGTGGTGTATTGCTGCCATGGCTGTGGCAGAGTCCAGTGGAGC 3228
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RESULT 7

US-09-600-776-5
; Sequence 5, Application us/09600776
; Patent No. 6326168
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: A novel potassium channel protein


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; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (263)...(1132)
; US-09-358-383C-7

Query Match      26.08; Score 844.4; DB 4; Length 1132;
Best Local Similarity 99.9%; Pred. No. 1.7e-168;
Matches 845; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCGGCCAATGGGGGCTCTCTGGCCCTCAGAACACCTTCTGTGACACCATCGGTACG 60
DB ATGCGGCCAATGGGGGCTCTCTGGCCCTCAGAACACCTTCTGTGACACCATCGGTACG 60
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QY 121 CCGGTGCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTAGGTC 180
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QY 541 CTGAGAGAGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
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QY 601 AACTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
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QY 721 ACTGTGCTTACAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
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QY 781 CCCAGCGTCTGTACCTGGCGGTGGAGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
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QY 841 CGTACC 846
DB |||||
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DB 1103 CGTACC 1108

RESULT 11
US-09-358-383C-17
; Sequence 17, Application US/09358383C
; Patent No. 6518398
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Kory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/09/358.383C
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USSN 09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 3321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3321)
; US-09-358-383C-17

Query Match      23.4%; Score 761.2; DB 4; Length 3321;
Best Local Similarity 62.2%; Pred. No. 6.7e-151;
Matches 1319; Conservative 0; Mismatches 708; Indels 93; Gaps 4;

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QY 121 CCGGTGCTACTGCTCTGTGAGCTTCTGTGACCTCACGGGCTTCTCCCGGCTGAGTGC 180
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QY 601 AACTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
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DB GCATTCGGGAGTATAAAGTTCTGATGCAAAAAGTCCAAATTCATCTCTCTCTCTCT
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QY 781 CCCAGCGCTGTGACCTGGCGGTGGAGTCCCTTCATCTTTCACATTTGACATTTGCTGTAATTC 840
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Db 1348 TTCTGCATCTGCACATGCTCATTTGGTTCCTTGATGACGCGCTTGGTGTGGGAAGCTG 1437
QY 1501 ACGGCATCATCCAGCGATGTAGCGCGCGCTTTCTGTACACACCGCCAGCGCGAGC 1560
Db 1408 ACAGCAATCACAGAGATGTACTCCAGATGGTCCCTCTATCACACTAGAAATGAAGAT 1467
QY 1561 CTGCGCGACTACATCCGATCCACCGTATCCCGAAGCCCTCAAGCAGCGCATGCTGGAG 1620
Db 1468 CTGAAGATTTTCATCCGTGCTCATCTACTTGCCTCCACAACTCAAGCAGAGAGTGTCTGAA 1527
QY 1621 TACTTCCAGGCACTGGCGGTGAACAAATGGCATCGACACCCAGCTGCTGCGAGGC 1680
Db 1528 TATTTTCAACAACCTGGTTCAGTCAACAATGGAATAGATTCAATGAGCTTTTGAAGAGC 1587
QY 1681 CTCCTGACGAGCTGCGCGCAGACATGCCCATGACCTGCAAGAGGAGTCTTCAGCTG 1740
Db 1588 TTTCAGATGAACCTGCTTCTGACATCACTATGCACTTGAACAAGAGATCTTACAGTTG 1647

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QY 1741 CCAGTGTGTAGCGCGCCAGCCGGGCTGCTGCGGCACACTGCTCTGCGCCCTGGCGCC 1800
Db 1648 TCCCTTTTGAATGTGCCAGCGGGGCTGCTGAGTCTCTGCTCTACACATCAAAACC 1707
QY 1801 GCCTTCTGACGCGCGGAGTACCTCATCCACCAAGGCGATGCCCTGCAAGCCCTCTAC 1860
Db 1708 TCTTCTGCTGCTGCGGGGAGTATCTGCTGCTCAAGGGGATGCTTTGAGCGCACTAC 1767
QY 1861 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
Db 1768 TTGTATGCTGCGGCTCCATGGAAGTCTTAAAGACAGCAGTGTGCTGCTGCTGCTGCTG 1827
QY 1921 AAGCGGACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
Db 1828 AAGGGATTTAATTGAGCAATCTATCAATTAAGCAAGTATCAAGACCAATGCA 1887
QY 1981 GAGTGAAGGGCTGAGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
Db 1888 GATGTAAAGGCTTTAAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1947
QY 2041 AGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
Db 1948 GTGCTAGACCTTTACCCAGCAATATGCTCACAATTCGTGAAGACATTCAGCATGACCTC 2007
QY 2101 AGCTACAACTGGGTGCTGG 2120
Db 2008 ACATAAACCTCCGAGAAG 2027

RESULT 12
US-09-358-383C-15
: Sequence 15, Application US/09358383C
: Patent No. 6518398
: GENERAL INFORMATION:
: APPLICANT: Curtiss, Rofy A.J.
: TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
: FILE REFERENCE: MNI-055CP
: CURRENT APPLICATION NUMBER: US/09/358,383C
: CURRENT FILING DATE: 1999-07-21
: PRIOR APPLICATION NUMBER: USSN 09/119,855
: PRIOR FILING DATE: 1998-07-21
: NUMBER OF SEQ ID NOS: 36
: SOFTWARE: Patent-In Ver. 2.0
: SEQ ID NO 15
: LENGTH: 5107
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (196)..(3516)
: NAME/KEY: misc_feature
: LOCATION: 4777
: OTHER INFORMATION: n = a,g,t or c
US-09-358-383C-15

Query Match: 23.4%; Score 761.2; DB 4; Length 5107;
Best Local Similarity 62.2%; Pred No. 7.5e-151;
Matches 1319; Conservative 0; Mismatches 708; Indels 93; Gaps 4;

QY 1 ATSCCGGCGATGCGGGGCTCTCTGCGGCTCAGAACACTTCTCTGGACACATCGCTACG 60
Db 196 ATGCGGGTTATGAAGGATTACTTGGCGCGCAAAACACTTCTCTGGACACATCGCCACC 255
QY 61 GCTTCGAGCGCACCCACASTAACTTCTGCTGGCAGCCGCCAGCTTCTCCGGGCTCTTC 120
Db 256 CGTTTGAAGCAACATAGCAACTTCACTCTGCCAATGCGGAGGTGGTAAGGGTTTC 315
QY 121 CCGTGGTCTACTGCTCTGATGGCTTCTGACCTCAGCGCTTCTCCGGGCTGAGGTC 180
Db 316 CCGATAGTCTACTGTTCCGATGGCTTCTGCGAGCTTCTGCGATTTGCGGACTGAAGTC 375
QY 181 ATSCAGCGGGGCTGTGCGCTGCTCTCTCTTATGGCGCAGACACAGTACGCTCGTCGG 240

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Db 376 ATGAGAGAGTGTGAGCTGCAAGTCTCTATTTGGGGTGAACCAATGAGCAACTGATG 435
Qy 241 CAACAGATCCGCAAGGCCCTGGAGCAGCAACAAGAGTCAAGGCTGAGCTGTATCTCTATC 300
Db 436 CTTCAANTAGAAAAGTCACTGGAGAGAAACAGAAATCAAGAGGAAATATGTTCTAC 435
Qy 301 CGGAAGAGGGGCTCCGGTCTGGTGTCTCTGGATGTGATACCCATAAAGATGAGANA 363
Db 496 AAGAAAACGGGCTCCATTTTGGTGTCTCTGGTGTCTCTGGTGTCTCTGGTGTCTCTGGT 555
Qy 361 GGGAGGTGGTCTCTCTCTCAAGAGACATCAGCGAATCAAGCAACCAAGAGGG 420
Db 556 GGAGATGTAGTACTTTTCTGGCTCGTTCAGAGATATACAGATA-CAAAAGTGAAGAT 624
Qy 421 GGCCTCCAGATGATGAGAGAGACAGGTGGTGGCGCGCCGATATGCGCGCAGCATCC 480
Db 615 TACTCCAGAGATATAAAGAACAAAGTCAAGGAAGATCAAGAGAGGAGCCCA--- 671
Qy 481 AAGGCTTCATGCCAACCGCGCGGAGCGGGCGGTGTCTACCACTGTCCGGGCAC 540
Db 672 -----CTTGACTCAGCGCGGAGAGCGAGTGGAGTCTTTATCACATCTCTGGGCAG 726
Qy 541 CTGAGAGAGCCCAAGGCGCAAGCAAGCTCAATTAAGGGGTGTTGGGGAGAAACCA 600
Db 727 CTCGAAAGAGAGAAAGACNAATCGAATAAATAACAAATGTTTGTAGATAACCA 736
Qy 601 AACTTGCTGAGTACAAGTAGCGGCCATCCGGAAGTGGCCCTTCACTCCCTGACTGT 660
Db 787 GCATTTCCGGAGTAAAGTTCTGATGCAAAAAGTCCAAATTCATCTCTGCAATTT 846
Qy 661 GGGCACTGAGAGCACTGGGATGGCTTCATCTGCTGCCACAGTCTATGCGGTG 720
Db 847 AGCACTTTAAAGCTGGCTGGGACTGGCTTATTTTGTGGCAAGCTTTTATGTTGCTGG 906
Qy 721 ACTGTGCCCTACAGCGTGTGTGAGACAGAGCGGAGCGGAGCGCGCGCGCGCGCG 780
Db 907 ACTGTACTTACAACGTTTGTCTTATTGGCAATGACGACCTGTCCCAACTCGGAGC--- 963
Qy 781 CCCAGCTGTGACCTGGCGGTGGAGGTGCTCTTCATCCTTGACATTTGCTGGAATTC 840
Db 964 ACAACCGTCACTGACATGTCAGTGGAGATTCTTTTATTATAGATATTATTTAAATTC 1023
Qy 841 CGTACCATTCTGTGCTCAAGTGGCGGAGTGTGTGTTGCCCAAGAGTCCATTTGCCCT 900
Db 1024 CGAACACTTATGTACGAACTGTGGCCAAAGTATCTTTGAAGCAAGATCAATTTGCAIC 1083
Qy 901 CACTAGTCAACCACTGGTCTGCTGGATGTATCCAGCGGTGGCCCTTTGACCTGCA 960
Db 1084 CACTATGTCAACCACTGGTCTGCTGGATGTATCCAGCGGTGTATCCCAACAGTACTACTG 1143
Qy 961 CATGCTTCAAGTCAAGCTGCTACTTCGGGGCCATCTGCTGAAGAGGTGGCGCTGCTG 1020
Db 1144 TATGCTTCAAGTCAAGCTGCTACTTCGGGGCCATCTGCTGAAGAGGTGGCGCTGCTG 1203
Qy 1021 GCGTGTGGCGCTGCTTCGGCGGTGGAGCGGTACTCGAGTACAGCGCGGTGGT 1080
Db 1204 GGTCTTTGGCTGCTGCAAGAGTGTAGACCGGTATTCGCCAAGTACTACTACTGCTG 1263
Qy 1081 ACATGCTCATGCGCTGTTGCGCCCTGCTCGGCACTGCTGCGCTGCTGCTGCTGCTG 1140
Db 1264 ACTGTGCTATGCTCATGTTTGGCACTGCTGCACTGCTGCACTGCTGCTGCTGCTGCTG 1323
Qy 1141 ATTGGCAGCGGAGATCGAGAGCGGAATCCGAGCTGCTGAGATGGCTGGCTGGCTGCA 1200
Db 1324 ATTGGAAAATGGAGAGAGAGACAGCGCTTCTGAAGTGGGAAGTGGTGGCTTCTAT 1363
Qy 1201 GAGTGGCGCCGCTGCTGAGACTCCCTACTACTGCTGGTGGCGGAGCGAGCTGGAGG 1260
Db 1384 GAGTTGGGAAGAGACTGGAATCTCCACTAT----- 1416
Qy 1261 AACAGCTCCGCGCAGATGACACTGACAGAGCAGCGAGCGGAGCGGAGCGGCTG 1320
Db 1417 -----GGCAAC 1422

Qy 1321 GAGTGTCTGGCGGCCGCTGCTGGCAGCGCCTACATACCTCCCTTACTTCCACTC 1380
Db 1423 AATACCTTGGGGGGCCGCTGATCCGAAGTGCCTATATTTGCGCTCTGTACTTCCACTG 1482
Qy 1381 AGCAGCTTCACAGAGGTGGCTGGCAAGCTGTCCGCCACAGCGGACCGAAGATC 1440
Db 1483 AGCAGCTTCACAGAGGTGGCTGGCAAGCTGTCTGTATACAGATGCAAGAAATC 1542
Qy 1441 TTCTCCATCTGCAACATGCTATGCGGCCCTGTATGACGCGGTGGTGTGGCAAGT 1500
Db 1543 TTCTCCATCTGCAACATGCTATGCGGCCCTGTATGACGCGGTGGTGTGGCAAGT 1602
Qy 1501 AGGCGCATATCCAGCGCATGTAGCCCGCGCTTCTGTATACAGAGCGGACCGCGAC 1560
Db 1603 ACAGCAATCATACAGAGATGTACTCCAGATGTCCTCTATACACTAGAAATGAT 1662
Qy 1561 CTGCGGACTACATCCGCTACCGGTATCCCAAGCCCTCAAGCAGCGCATCTCGAG 1620
Db 1663 CTGAAGATTTTATCCGCTGCTATCCTTGGCCCAACACTCAAGCAGAGATCTCGAA 1722
Qy 1621 TACTTCCAGGCGCCTGGCGGTGAACAATGGCATCGACACCGCGCTGCTCAAGC 1680
Db 1723 TATTTTCAACAACCTGCTGCTAGTCAACAATGAATAGATTCAATGAGCTTTTGAAGAC 1782
Qy 1681 CTCCCTGAGAGCTCGCGCAGACATCGCCATGACCTGACAGAGAGGTCTCGACGTG 1740
Db 1783 TTTCAGATGAATCGTCTTACATCACTATGCACTTGAACAAGAGATCTTACAGTTG 1842
Qy 1741 CCACCTGTTGAGGGCGCGCGCTGCTGGGGGCTGCTCTGCGCCCTCGCGCC 1800
Db 1843 TCCCTTTTGAATGTGCCAGCGGGGCTGCTCAGGTCTCTCTACATCAAAACC 1902
Qy 1801 GCTTCTTCACCGCCGCGAGTACCTCATCCACCAAGCGATGCGCTGACAGCGCTCTAC 1863
Db 1903 TCTTCTGTGCTCGGGGAGTATCTGCTGGTCAAGCGGATGCTTTCAGGCGCATCTAC 1962
Qy 1861 TTGTCTGCTGCTGCTGCTGAGGTGCTCAAGGTGCGCGCTGCTGCGCCATCTAGGG 1920
Db 1963 TTGTATGCTGCGGCTCCATGGAGTTCTTAAAGACAGCATGCTGCTGGCTATTTGGG 2022
Qy 1921 AAGGCGCACTGTATCGCTGTGAGTGGCGCGGAGAGAGGTGTTAAAGCGCAATGCC 1980
Db 2023 AAAGGGATTAAATTTGGAGCAATCTATCAATTAAGGACCAAGTATCAAGCAATGCA 2082
Qy 1981 GAGTGAAGGGCTGAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
Db 2083 GATGTAAAGGGTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2142
Qy 2041 AGCCTTGGCTGTACCCCGAGTTTCCCGCGCTTACGTGCTGCTGCTGCTGCTGCTGCTG 2100
Db 2143 GTGCTAGACCTTTACCCAGATATGCTCACAATTCGTTGGAAGACATTCAGCATGACCTC 2202
Qy 2101 AGCTACAACCTGGGTGCTG 2120
Db 2203 ACATACAACCTCCGAGAAG 2222

RESULT 13

US-09-358-383C-6
; Sequence 6, Application US/09358383C
; Patent No. 6518398
; GENERAL INFORMATION:
; APPLICANT: CURTIS, RORY A. J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/09/358,383C
; CURRENT FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USN 09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6

: LENGTH: 1626
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(1626)
US-09-358-383C-6

Query Match 17.6%; Score 572.8; DB 4; Length 1626;
Best Local Similarity 61.8%; Pred. No. 2e-111;
Matches 1034; Conservative 0; Mismatches 547; Indels 93; Gaps 4;
QY 1 ATGCGGCGCATGGGGCTCTGGCGCTCAGACACCTTCTGGACACCATCGCTAGG 60
DB 1 ATGCGGCTTATGAAGGATTACTGGCGCGCAAAACACCTTCTGGACACCATCGCCACC 60
QY 61 CGCTTCGACGGCAGCACAGTAACCTTGGTCTGGGCAAGCCGAGGTGGCGGGTCTTC 120
DB 61 CGTTTTCGCGAACACATAGCAACTTCATCTTGCATGCCCAGGTGCTTAAGGTTTC 120
QY 121 CGCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTACGGGCTTCTCCGGGCTAGGTC 180
DB 121 CCATAGTCTACTGTTCGATGGCTTCTGCGAGCTTGTGGAATTTGCCCGAACTGAAGTC 180
QY 181 ATGCGCGGGCTGTGCTCTTCTTATGGCGCCAGACACCACTGAGCTGCTCCGC 240
DB 181 ATGCAGAGAGTGTAGCTGCAAGTCTTATTTGGGTTGAAACCAATGAGCACTGATG 240
QY 241 CAACAGATCCGAAGGCCCTGGACGAGCACAGAGATTCAGGGCTGAGCTGATCTGAC 300
DB 241 CTTCAAAATGAAAGATCACTGCGAGGAGAAACAGAAATTCAGAGGAGAAATTAATTTCTAC 300
QY 301 CGGAGAGGGGCTCCGCTCTGGTGTCTCTCTCTGATGATACCCATTAAGATAGAGAA 360
DB 301 AGAGAAAGGGGTCTCCATTTGGTGGCTACTGGATATGCTTCCATTAAGAAATGAAAAA 360
QY 361 GGGGAGGTGGCTCTCTCTAGTCTCTACAGGACATCAGCGAAACCAAGAACCGAGG 420
DB 361 GGAGATGATGATTTTCTGGCTCGTTCAAGATATTAACAGATA-CAAAAGTAAGAT 414
QY 421 GCGCCGAGAGATGGAAGAGAGAGTGGTGGCGCGCGGATATGCGGGGCA-ATGACC 480
DB 420 TACTCCAGAGATTAAGAAAGAGACAAAGTCAAGGAAGATCAAGAGCAGGACCCA... 476
QY 481 AAAGCTTCANTGCCAACGCGCGGAGCGCGGCTGCTCTACACCTGTCCGGGAC 540
DB 477 -----CTTTGACTCAGCCCGGAGCGGATCGAGGAGTCTTTATACACATCTCTGGGAC 531
QY 541 CTGCGAAGCAGCCCAAGGCAAGCACAAGCTCAATAAGGGGTGTTTGGGAGAGAACCA 600
DB 532 CTGCAAGAGAGAAAGAACAAATGAAATTAATTAACAANTGTTTGTAGATAACCA 591
QY 601 AACTTGCCTGAGTACAAAGTAGCGCCATCCGGAAGTGGCCCTTATCTGTGTGCACTG 660
DB 592 GCATTTCCGGAGTATAAGATTTCTGATGCAAAAAGTCCAAATTCATACCTTCTGCAATTT 651
QY 661 GGGCACTGAGACCCAGCTGGATGCTTCATCCCTGCGCCACACTCTAIGTGCCTGTC 720
DB 652 AGCACTTTTAAGCTGGCTGGGACTGGCTTATTTGTGGCAACGTTTATGTGCTGCTG 711
QY 721 ACTGTGCCCTACAGCGTGTGTGAGCAGCAGCGGAGCCGACCTGCGCCCGCGCGCG 780
DB 712 ACTGTACCTTACACGTTTCTTATTTGCAATGAGCACTGTCCACACTCGGAGC--- 768
QY 781 CCAGGCTGTGACTGCGCGTGGAGTCCCTTCATCTTACATCTTGACATTTGCTGTAATTC 840
DB 769 ACAACCGTCAGTACATTCGAGTGGAGATCTTTTATTATAGATATTTTAAATTTTC 828
QY 841 CGTACCACATTTGCTCCAAAGTCGGCGCAGGTGGTGTTCGCCCAAGTCCATTTGCCCTC 900
DB 829 CGAACCAACTTATGTACGAAGTCTGGCCAAAGTATCTTTTAAAGCAGAGATCAATTTGCATC 888
QY 901 CACTAGCTCACCACCTGGTTCCTGCTGGATGTCTATCGCAGCGCTGCCCTTTCACCTGCTA 960

DB 889 CACTATGTCACAACTTGGTTCATCATTTGATTATTCGCTGCCCTTGCCCTTGTCTCTG 948
QY 961 CATGCTTCAAGTCAACAGCTGTACTTGGGGGCCCACTTGTGTGAAGAGCGTGGCGCTCTG 1020
DB 949 TATGCTTCAAGTCAACAGTGTCTCTGCTGAGTCTTCTTAAGAGCAGTGGCGCTCTG 1008
QY 1021 CGCTGTGCGCTGCTTCCGGCTGGACCGGTACTCGAGTACAGCGCGCGGTGGTCTGCTG 1080
DB 1009 CGTCTTTTGGCTCTGCTGCGAGAGTTAGACCGCTTATTCACCAACACAGTATATGCTG 1068
QY 1081 ACATGCTCATGGCGCGTGTTCGCCCTGCTGCGCACTGGGTGCGCTGGCTGGTGTGTTAC 1140
DB 1069 ACTGCTCATGTCCTATGTTGCACTCTTGCACACTGGATGGCGGTGATCTGTGAGCTC 1128
QY 1141 ATTGCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCTGAGATTTGCTGCTOCAG 1200
DB 1129 ATTGAAAAATGGAGGAGGAGAACACAGCGCTTCTGAAGTGGGAAGTTGTTGCTTCAT 1188
QY 1201 GAGTGGCGCCCGCACTGGAGACTCCCTACTACTACCTGTTGGCCGAGACCGAGCGG 1260
DB 1189 GAGTTGGGAAAGAGACTGGAACTCTCCATACTA----- 1220
QY 1261 AACAGCTCCGCCAGAGTGACAACCTGCAGCAGCAGCAGCGAGCGCAACCGGCGCTG 1320
DB 1221 -----TGGCAAC 1227
QY 1321 GAGTGTGTGGCGGCCGCTGCTGCGCAGCGCTACATACCTCCCTCTACTTGCCTC 1380
DB 1228 AATACCTTGGGGCGCGCTCGATCCGAAGTGCCTATATGCGGCTCTGTACTTCACGCTG 1287
QY 1381 AGCAGCTCAGCAGCGGTGGGCTTGGCAACGTGTCGCCACAGCGACACGAGCAATC 1440
DB 1288 AGCAGCTCAGCAGCGGTGGGTTTGGGAACGTCTCTGCTAATACAGATGCCAGAAAGATC 1347
QY 1441 TCTCCATCTGCACATGCTCTCATGCGGCGCTGATGACGCGGTGGTGTGGGAACGTG 1500
DB 1348 TCTCCATCTGCACATGCTCTCATGCGGCGCTGATGACGCGCTTGTGTTGGGAACGTG 1407
QY 1501 AGGCGCATCTCCAGCGCATGACGCGCGCGCTTCTGTACCACAGCGCGACCGCGAC 1560
DB 1498 ACAGCAATCATACAGAGGATGCTAGTCCAGATGTCCTCTAICACACIAGAACATAGGAT 1467
QY 1561 CTGCGGACTACATCCGATCCAGCGTATCCCAAGCCCTCAAGCAGCGCATCTGGAG 1620
DB 1488 CTGAAGATTTCATCCGCTGCTCATCTACCTGCCCCAACACTCAAGCAGAGATGCTCGAA 1527
QY 1621 TACTTCCAGGCACTGGCGCGGTGAACAA1GGCATCGACACCGCAGCTGCTG 1674
DB 1528 TATTTCAACAACCTGTGTCAGTCAACATGGAATAGATTCAATGAGGTAATG 1581

RESULT 14
US-09-358-383C-4
: Sequence 4, Application US/09358383C
: Patent No. 5518398
: GENERAL INFORMATION:
: APPLICANT: Curtis, Rory A.J.
: TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
: FILE REFERENCE: MNI-055CP
: CURRENT APPLICATION NUMBER: US/09/358.383C
: CURRENT FILING DATE: 1999-07-21
: PRIOR APPLICATION NUMBER: USSN 09/119.855
: PRIOR FILING DATE: 1998-07-21
: NUMBER OF SEQ ID NOS: 36
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 4
: LENGTH: 2694
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (215)..(1840)

US-09-358-383C-4

Query Match 17.6%; Score 572.8; DB 4; Length: 2694;
Best Local Similarity 61.8%; Pred. No. 2.3e-11;
Matches 1034; Conservative 0; Mismatches 547; Indels 93;

QY	1	ATCGCGCCATCGGGGGCTTCCTGGCGCTCAGAACACACCTTCTCTGGACACCATCGCTAGG	60
DB	215	ATCCGGTTTAAAGAGGNTTACTGGCGCGCAAAACACCTTCTGACACCATCGSCACG	274
QY	61	CGCTTCGACGGCACGCACAGTAACCTTCGTGCTGGCAAGCCGACAGTGGCGGCGCTTTC	120
DB	275	CGTTTGAAGGAACACATAGCAACTTCATCCTTGCCTAATGCCAATGCCAGGTTC	334
QY	121	CCCGTGGTCTACTGCTCTGATGCGTCTCTGTGACCTCAGGGCTTCTCCGGGCTGAGGCTC	180
DB	335	CCCATAGCTACTGTTCCGATGGCTTCGCGAGCTTGCCTGATTTCCGCGCAATCGAAGCTC	394
QY	181	ATCGACGGGGCTGTGCTGCTCTCTTCTTTAATGGCCAGACACCAAGTCAGTTCGCTCGC	240
DB	395	ATCAGAGAAGTTGTACTCTCAAGTTCCTATTTTGGGCTTGAACCAATGAGCAACATG	454
QY	241	CAACAGATCCGAAGGCCCTGGAGAGCACACAGGATTTCAAGCTGAGCTGATCTCTGTAC	300
DB	455	CTTCAAAATGAAAGTCACTGGAGAGAAACAGAAATCAAAAGGAGAAATATGTTCTAC	514
QY	301	CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCCTGGATGTGATACCCATAAAGAAATGAGAA	360
DB	515	AAGAAAAACGGTCTCCATTTTGGTGGCTACTGGATATGCTCCCATAAAGAAATGAAAA	574
QY	361	GGGGAGTGGCTCTCTTCTTAGTCTCTCAGACGACATCAGCAAAACCAAGACCGAGGG	420
DB	575	GGAGATGTAGTACTTTTCTGGGCTGGTTCAAAGATATAACAGATA-CAAAAGCTGAAGAT	633
QY	421	GGCCCCACAGATGGAAGGAGACAGGTGGTGGCGCGCGCGATATGCCGGGCACCATCC	480
DB	634	TACTCCAGAAGATAAANAAGAACAAAGTCAAGGAAGATCAAGACGAGGCCCA---	690
QY	481	AAAGGCTTCAATGCCAACCGCGCGGAGCGGGCGGTGCTTACACCTGTCCGGGCGAC	540
DB	691	-----CTTTGACTCAGCGCGGAGCGAGTGCAGCAGTCTTTATCACATCTCTGGGCAC	745
QY	541	CTGCAGAAGCAGCCCAAGGCGCAGCAACAGCTCAATAAAGGGGTGTTTGGGAGAAACCA	600
DB	746	CTGCAAAGACAGAAAGACACAAATTGAAATAAATCAACATGTTTGTAGATAACCA	805
QY	601	AACCTGGCTGAGTACAAGTAGCGGCCATCGGAAGTCGCCCTTCATCTGTTGTGCACGT	660
DB	806	GCATTTCCGGAGTAAAGTTCTGATGCAAAAAGTCCAAATTCATCTTCGTGCACTTT	865
QY	661	GGGCACTGAGAGCCACCTGGATGGCTTCATCTGCTCGCCACACCTCTATGTGGGTGTC	720
DB	866	AGCACTTTAAAGCTGCTGGACTGGCTTATTTGTTGGCAAGTTTATGTTGCTGTG	925
QY	721	ACTGTGCCCTACACGTTGTGTTGAGCACAGCAGCGAGCCAGTGCAGCGCCCGGCCG	780
DB	926	ACTGACTCTACAAGTTGCTTTATTGGCAATGACCAACCTGTCCCAACTCGGAGC---	982
QY	781	CCCAGCGTCTGTACCTGGCGCGTGGAGGTCTCTTCATCTTGACATGTGCTGAATTTC	840
DB	983	ACAACCGTCACTGACA-TGCCAGTGGAGATCTTTTATTAGATATTATTTAAATTC	1042
QY	841	CGTACCACTTCTGTGTCAGAGTCGGGCGAGTGGTGTTCGCTCAAAAGTCCATTTGCTC	900
DB	1043	CGAACAACITATGTCAGCAAGCTGCGCAAGTTATCTTTGAAGCAACATCAATTGTCATC	1102
QY	901	CACTAGCTCACCACTGGTTCCTGCTGGATGTCAATGAGTGCAGCGTGCCTTTGACCTGC	960
DB	1103	CACATGTCAACAACCTGTTCACTATGATTTAATCGCTGCCCTGCCCTTTGATCTCTG	1162
QY	961	CATGCTTTCAAGGTCAACGTGTACTTCCGGGCCCATCTGCTGAAGACGGTGCCTGCTG	1020
DB	1163	TATGCTTTCAAGCTCACAGTGGTGTCTCTGTGATCTCTTAAAGACAGTGCCTGCTG	1222

Qy	1021	CGCTGCTGCGCCCTGCTTCGCGCGCTGGACCGGCTACTCCAGTACAGCCCGCTGCTGCTG	1582
Db	1223	CGTCTTTTTCGCTGCTGCTCAGAAAGTTAGACCGGTATTCCACACAGTACTATCGTCTG	1282
Qy	1081	ACACGTCTCATGGCCGCTTTCGCGCTGCTGGCGCACTGGGTGCGCTCGCTGCTGCTGTTTAC	1140
Db	1283	ACTGCTGCATGTCATGTTTTCGACTCTCTTGCACACTGATGATGCGCTGATCTCGTAGCTC	1342
Qy	1141	ATTTGCCAGCGGGAGTCGAGACGAGCAATCCGAGCTGCTGAGATTTGGCTGCTGCTGAG	1200
Db	1343	ATTGGAAAAATGGAGAGGGAGAACACAGCCTTCTGAAGTGGGAAAGTTGTTGGCTTCA	1402
Qy	1201	GAGCTGGCGCCCGCCACTCGAGACTTCCCTACTACTCTGGTGGCGCGGAGCGCACTGGAGGG	1260
Db	1403	GAGTTGGGAAGAGACTGGAATCTCCACTA	1454
Qy	1261	AACAGCTCCGCGCAGAGTGACACTGCAAGCAGCAGCGGAGGCAACGGGATGGGGCTG	1320
Db	1435	-----TGGCAAC	1441
Qy	1321	GAGCTGCTGGCGGCGCGCTCGCTGCGCAGCGCTACATCACTGCTCTTACTTCGCATC	1380
Db	1442	AAATCTTTGGGGCGCGCTGATCCGAGTGCCTATATTGCGCTCTGCTACTTCAGCTG	1501
Qy	1381	AGCAGCTCACCAGCGTGGGCTTGGCAAGCTGTCGCCAACAACCGACACCGAGAAGATC	1440
Db	1502	AGCAGCTCACCAGCGTGGGCTTGGCAAGCTGTCGCCAACAACCGACACCGAGAAGATC	1561
Qy	1441	TCTCCATCTGCACCATGCTCATCGCGCGCCCTCATGACGCGGCTGGTGTITGGGAAGCTG	1500
Db	1562	TCTCCATCTGCACCATGCTCATGATGGTGCTTGTATGACGCGCTTGGTGTITGGGAAGCTG	1621
Qy	1501	ACGGCATCATCCAGCGGATGATAGCGCGCGCTTTCTGTACACAGCGGACACGCGGAC	1560
Db	1622	ACAGCAATCATACAGAGGATGTACTCCAGATGGTCCCTCTATCACACTAGAAGAT	1681
Qy	1561	CTGCGGACTATCCCGCATCCACCGTATCCCAAGCCCTCAAGCAGCGATGCTGGAG	1620
Db	1692	CTGAAGATTTATCCCGTGCTCATCACTTCCCCCAACACTCAAGCAGGATGCTGGA	1741
Qy	1621	TACTTCCAGGCGCATGGCGGTTGAACAATGGCATGCACACCGAGCTGCTG	1674
Db	1742	TATTTCAACAACCTGCTGCTCAGTCAACAATGGAATGATTCAATGAGGTAATG	1795

RESULT 15
 US-09-358-383C-14
 : Sequence 14, Application US/09358383C
 : Patent No. 6518398
 : GENERAL INFORMATION:
 : APPLICANT: Curtis, Rory A.J.
 : TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
 : FILE REFERENCE: MNI:055CP
 : CURRENT APPLICATION NUMBER: US/09/358,383C
 : PRIOR FILING DATE: 1999-07-21
 : PRIOR APPLICATION NUMBER: USSN 09/119,855
 : PRIOR FILING DATE: 1998-07-21
 : NUMBER OF SEQ ID NOS: 36
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 14
 : LENGTH: 5955
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : FEATURE:
 : NAME/KEY: exon
 : LOCATION: (196)..(1770)
 : NAME/KEY: intron
 : LOCATION: (1771)..(2618)
 : NAME/KEY: exon
 : LOCATION: (2619)..(4364)
 : OTHER INFORMATION: At position 5625, n-any nucleic acid
 US-09-358-383C-14

Query Match		17.6%	Score 572.8;	DB 4;	Length 5955;
Best Local Similarity		61.8%	Pred. No. 2.9e-111;		
Matches 1034;		Conservative	0;	Mismatches 547;	Indels 93; Gaps 4;
Qy	1	ATCGCGGCTATGGGGGCTCTCGGGGCTTCAGACACACCTTCTCGACACCATCGGTAGC	60		
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Qy	61	CGCTTGACGCGACGACAGTAATTCGTCTGGCAAGCCGACGCTGGGGGCTCTTC	120		
Db	256	CGTTTGACCGGACACATACAACTTCATCTTGGCAATGCCAGGTGGCTAAGGGTTTC	315		
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Qy	241	CACAGATCCGCAAGGCGCTGGACGACCAAGAGTTCAAGCTGAGCTGATCTGTAC	300		
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Qy	361	GGGAGGTGCT	420		
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Qy	721	ACTGTGCTTACAGCTGTGTGTGACGACAGCGGAGCCAGTGGCGCGGCGCGCGG	780		
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Qy	781	CCCAGCTCTGTACCTGGCGGTGGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	840		
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Search completed: October 1, 2003, 21:16:56
Job time : 231 secs

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Qy	1141	ATTGCCAGCGGAGATCGAGGAGCGAA:CCGAGGCTGCTGAGATTGCTGCTGCTGCTG	1200
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GenCore version: 5.1.6
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OM nucleic - nucleic search, using sw mode:

Run on: October 1, 2003, 19:33:31 : Search time 788 Seconds
(without alignments)
10527.167 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1708419 seqs, 1275431651 residues
Total number of hits satisfying chosen parameters: 3416638

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

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17: /cgn2.6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3252	100.0	3323	10	US-09-965-830-1 Sequence 1, Appli
2	3245.8	99.8	3249	14	US-10-160-224-2 Sequence 2, Appli
3	3218	99.0	3857	14	US-10-121-746-19 Sequence 19, Appli
4	3156	97.0	3355	9	US-09-119-855-1 Sequence 1, Appli
5	3156	97.0	3355	14	US-10-185-867-1 Sequence 3, Appli
6	3153	97.0	3249	14	US-10-185-867-3 Sequence 3, Appli
7	3144	96.7	3240	9	US-09-119-855-3 Sequence 3, Appli
8	2664.8	81.9	3715	10	US-09-965-830-9 Sequence 9, Appli
9	869.8	27.2	3064	10	US-09-965-830-5 Sequence 5, Appli
10	869.8	26.7	3736	10	US-09-965-830-10 Sequence 10, Appli
11	844.4	26.0	870	9	US-09-119-855-9 Sequence 9, Appli
12	844.4	26.0	870	14	US-10-185-867-9 Sequence 9, Appli
13	844.4	26.0	1132	9	US-09-119-855-7 Sequence 7, Appli
14	844.4	26.0	1132	14	US-10-185-867-7 Sequence 17, Appli
15	761.2	23.4	3321	14	US-10-185-867-17 Sequence 15, Appli
16	761.2	23.4	5107	14	US-10-185-867-15 Sequence 15, Appli

17	572.8	17.6	1626	9	US-09-119-855-6 Sequence 6, Appli
18	572.8	17.6	1626	14	US-10-185-867-6 Sequence 6, Appli
19	572.8	17.6	2694	9	US-09-119-855-4 Sequence 4, Appli
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ALIGNMENTS

US-09-965-830-1
Sequence 1, Application US/09965830
Patent No. US2002017201A1
GENERAL INFORMATION:
APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
TITLE OF INVENTION: A novel potassium channel protein
FILE REFERENCE: Y9903-PTC
CURRENT APPLICATION NUMBER: US/09/965,830
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: 09/600,776
PRIOR FILING DATE: 2001-07-21
PRIOR APPLICATION NUMBER: JP P1998-346198
PRIOR FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 3323
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (6)...(3257)
US-09-965-830-1

Query Match 100.0%; Score 3252; DB 10; Length 3323;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1861 TTGTGTGCTCTGGCTCCATGGAGGTGCTTCAAGGGTGGCACCGTCTCTGCCATCTAGG 1920
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Qy 1921 AAGGGGACCTGATGGCTGTGAGCTGCCCCGGCGGAGCAGTGGTAAAGGCCAATGCC 1980
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Qy 2281 TCATCTCTAGCTGCCAGGTGCTATCCCACTGCGAACAGCAGCCGCGCTGCTAGGT 2340
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Qy 2341 GGCAGAGGAGGCGCAGGCGGAGGCTTTGAAGGCTGAGGCTGGGCCCTCTGCTGCT 2400
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RESULT 3
US-10-121-746-19
: Sequence 19, Application US/:0121746
: Publication No. US20030036648A1
: GENERAL INFORMATION:
: APPLICANT: Miller, Andrew P.
: APPLICANT: Curran, Mark Edward
: APPLICANT: Hu, Ping
: APPLICANT: Ruter, Marc
: APPLICANT: Wang, Jian-Wang
: TITLE OF INVENTION: No. US20030036648A1el Human Potassium Channels
: FILE REFERENCE: SEQ-15P
: CURRENT APPLICATION NUMBER: US/10/121,746
: PRIOR FILING DATE: 2002-04-11
: PRIOR APPLICATION NUMBER: US/09/336,643A
: PRIOR FILING DATE: 1999-06-18
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
: PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
: PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826
: PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
: NUMBER OF SEQ ID NOS: 87
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 19
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: TYPE: DNA
: ORGANISM: H. sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (249)...(3495)
: OTHER INFORMATION: K+Hnov14
US-10-121-746-19

Query Match 99.0%; Score 3218; DB 14; Length 3857;
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Db 546 CGGAAGAGCGGCTTCCGCTTCTGCTGCTGATGTATACCCATAAAGAAATGAJAA 605
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; CURRENT FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3355
; TYPE: DNA
; ORGANISM: Monkey
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (113)..(3352)
US-09-119-855-1

Query Match 97.0% Score 3156; DB 9; Length 3355;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 3192; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

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DB 464 GGGAGGTGGCTCTCTCTAGTCTCTACAGAGACATCAGTGAACCAAGAACCGAGGG 523
QY 421 GCGCCCGACAGATGGAAGAGACAGGTGGTGGCGGCGCGGATATGGCGGGCAGATCC 480
DB 524 GCGCTGACACAGTGAAGAGACAGGTAGTGGCGGCGCGGATATGGCGGGCAGATCC 583
QY 481 AAAGGCTTCAATGCCACCGCGGCGGAGCGGCGGTGTCTTACCACTCTCGGGGAC 540
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DB 1964 TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGGTGGCAGCGTGTCTGCGCCATCTAGGG 2023
QY 1921 AAGGGGACCTGATCGGCTGTGAGCTGCGCCCGCGGAGCAGGTGGTAAAGGCCAATGCC 1980

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Db	524	GGCCCTGACAGATGAAGGACAGAGTAGTGGCGGCGCGGATATGCGCGGACGATCC	583	
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Qy	541	CTGCAGAGGACGCCCAAGGCGAAGCAAGCTCAATAAGGGGGTGTTGGGAGAAACCA	600	
Db	644	CTGCAGAGGACGCCCAAGGCGAAGCAAGCTCAATAAGGGGGTGTTGGGAGAAACCA	703	
Qy	601	AAC TTGCTGAGTACAAAGTAGCGGCATCGGGAAGTCGCCCTTCATCCCTGTTGCACTGT	660	
Db	704	AAC TTGCTGAGTACAAAGTAGCTGCCATCGGGAAGTCGCCCTTCATCCCTGTTGCACTGT	763	
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Qy	721	ACTGTGGCTACAGCGTGTGTGTGAGCACACGAGGAGCGCACTGCGCGCGCGCGG	780	
Db	824	ACC GTGGCTTACAGCGTGTGTGTGAGCACACGAGGAGCGCACTGCGCGCGCGCGCA	883	
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Qy	901	CAC TACGTACCACTGGTCTGCTGGATGTCTACGAGGCTGCGCTTGACCTGCTA	960	
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Qy	961	CATGCCCTTCAAGGTCACAGTGTACTTCGGGCGCCATCTGTGAAGAGCGTGCCTGCTG	1020	
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Db	1784	CTCCTGACGAGTGGCGCAGACATCGCCATGCACCTGCACAAGAGAGTCTCTGCAGCTG	1843
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Db	1904	GCCTTCGACGCGGGCGAGTACCTCATCCACCAAGCGATGCGCTCGAGGCGCTCTAC	1963
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Db	1964	TTTGTCTGCTCTGGCTCCATGGAGTGCTCAAGGTTGGCACCGTGTCCCATCTCTAGG	2023
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Qy	2041	AGCCTTCGGCTTACCCCGAGTTTGGCCCGGCTTCACTCGTGGGCTCGAGGGAGCTC	2100
Db	2144	AGCCTTCGGCTTACCCCGAGTTTGGCCCGGCTTCACTCGTGGGCTCGAGGGAGCTC	2203
Qy	2101	AGCTACAACCTGGTGCTGGGGGAGGCTCTGCAGAGTGGACACAGCTCCCTGACGGC	2160
Db	2204	AGCTACAACCTGGTGCTGGGGGAGGCTCTGCAGAGTGGACACAGCTCCCTGACGGC	2263
Qy	2161	GACAATACCTTTATGTCACCGTGGAGGAGAGACAGATGGGAGCAGGCGCCACG	2220
Db	2264	GACAATACCTTTATGTCACCGTGGAGGAGAGACAGATGGGAGCAGGCGCCACG	2323
Qy	2221	GTCTCCCGACCCAGCTGATGAGCCCTCCAGGCCCTGCTGTCCCTGGCTGCACCTCC	2280
Db	2324	GTCTCCCGACCCAGCTGATGAGCCCTCCAGGCCCTGCTGTCCCTGGTTCACCTCC	2383
Qy	2281	TCATCTCTAGCTGCCAAGTGCCTATCCCAAGTCGACACAGCACCCCGGCTGTCTAGT	2340
Db	2384	TCATCTCTAGCTGCCAAGTGCCTATCCCAAGTCGACACAGCACCCCGGCTGTCTAGT	2443
Qy	2341	GGCAGAGGGAGGCCAGGCGCAGGGGCTTTGAAGCTGAGGCTGCGCCCTCTGCTCC	2400
Db	2444	GGCAGAGGGAGGCCAGGCGCAGGGGCTTTGAAGCTGAGGCTGCGCCCTCTGCTCC	2503
Qy	2401	CCAGGGCCCTACAGGGGCTACGGCTGCCCGCCCATGCCATGCCATGGAAATGCCCCAGATCTG	2460
Db	2504	CCAGGGCCCTACAGGGGCTACGGCTGCCCGCCCATGCCATGGAAATGCCCCAGATCTG	2563
Qy	2461	AGCCCCAGGCTAGTAGATGSCATTGAAGAGGGCTGTGGCTCGGACAGCCCCAAGTTCTCT	2520
Db	2564	AGCCCCAGGCTAGTAGATGSCATTGAAGAGGGCTGTGGCTCGGACAGCCCCAAGTTCTCT	2623
Qy	2521	TTCCGGTGGGCCAGTCTGGCCCGGGAATGTAGCAGCAGGCCCTCCCTCGACAGAGC	2580
Db	2624	TTCCGATGGGCCAGTCTGGCCCGGGAATGTAGCAGCAGGCCCTCCCTCGACAGAGT	2683

QY 2581 GGCCTGCTCACTGTTCCTCCATGGGCCGACGAGGCAAGACACAGACACACACTGACAAAG 2640
Db 2684 GGCCTGCTCACTGTTCCTCCATGGGCCGACGAGGCAAGACACACAGACACACTGACAAAG 2743
QY 2641 CTTGGCAGGGGTACACAGCTGTTCAGACAGGTGTCTGACAGATGCGGGAGAGACTGACAG 2700
Db 2744 CTTGGCAGGGGTATGAGAGCTGTTCAGACAGGTGTCTGACAGATGCGGGAGAGACTGACAG 2803
QY 2701 TCACCTCCACAGGTGTTCAGAGCTGTTCGCGGCCACAGGAGGCTCCGTGCGCTGG 2760
Db 2804 TCACCTCCACAGGTGTTCAGAGCTGTTCGCGGCCACAGGAGGCTCCGTGCGCTGG 2863
QY 2761 GCATCGGAGAGGGGCGGTGCGCAGCAGACACCTCGGGGCTTCGACAGCTGTGTGTG 2820
Db 2864 GCCTCAGGAGAGGGGCCATGCCAGCCAGCACCTCCGGGCTTCGACAGCTGTGTGTG 2923
QY 2821 GACACTGGGGATCCTCCTACTGCTGACGCCCCAGCTGCTGTCTGAGTGGGACT 2880
Db 2924 GACACTGGGGATCCTCCTACTGCTGACGCCCCAGCTGCTGTCTGAGTGGGACT 2983
QY 2881 TGGCCCCACCTCGTCCGGGGCTCCTCCCTCATGGCACCTGGCCCTGGGGTCCGCCA 2940
Db 2984 TGGCCCCACCTCGTCCGGGGCTCCTCCCTCATGGCACCTGGCCCTGGGGTCCGCCA 3043
QY 2941 GCGTCTCAGAGTCCCTCGCTGGCTGAGCCACAGCTTCTTGAGACTCCACCTCAGACTCA 3000
Db 3044 GCATCTCAGAGTCCCTCGCTGGCTGAGCCACAGCTTCTTGAGACTCCACCTCAGACTCA 3103
QY 3001 GAGCCCCCTGCTCAGGAGACTCTGCTCTGAGCCACACCTCGCTCCCTCGCTCCT 3060
Db 3104 GAGCCCCCTGCTCAGGAGACTCTGCTCTGAGCCACACCTCGCTCCCTCGCTCCT 3163
QY 3061 TCTGAGGAGGGGTAGGACTGGGCCCGCAGAGGCTGTGAGCCAGGCTGAGGCTACACAGC 3120
Db 3164 TCTGAGGAGGGGTAGGACTGGGCCCGCAGAGGCTGTGAGCCAGGCTGAGGCTACACAGC 3223
QY 3121 ACTGAGAGCCCCACAGGCTCAGGGGGCTTGCGCTTGCGCTGGACCCACAGGCTG 3180
Db 3224 ACTGAGAGCCCCACAGGCTCAGGGGGCTTGCGCTTGCGCTGGACCCACAGGCTG 3283
QY 3181 GAGATGGTCTATTGGTGGCATGGCTCTGACAGTCCAGTGGACCCAGGAGAGAGG 3240
Db 3284 GAGATGGTCTATTGGTGGCATGGCTCTGACAGTCCAGTGGACCCAGGAGAGAGG 3343
QY 3241 ACAGGGGTCTGA 3252
Db 3344 ACAGGGGTCTGA 3355

RESULT 6

US-10-185-867-3
; Sequence 3, Application US/10185867
; Publication No. US20030104429A1
; GENERAL INFORMATION:
; APPLICANT: Curtius, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/10/185,867
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US/09/358,383
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USSN 09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 3249
; TYPE: DNA
; ORGANISM: Macaca sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3249)
US-10-185-867-3

Query Match: 97.0%; Score 3153; DB 14; Length 3249;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 3189; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
QY 1 ATCCGGCCATCGGGGCTTCCTGGGCGCTCAGAACACTTCTCGACACCATCGCTGACG 60
Db 1 ATCCGGCCATCGGGGCTTCCTGGGCGCTCAGAACACTTCTCGACACCATCGCTGACG 60
QY 61 CGCTTCACGCGCAGCAGCACTAACTCGTCTGGCAACCCCGAGGTGGCGGGCTCTTC 120
Db 61 CGCTTCACGCGCAGCAGCACTAACTCGTCTGGCAACCCCGAGGTGGCGGGCTCTTC 120
QY 121 CCGCTGTCTACTGCTCTGATGGCTTCGTGAGCTTCACGGGCTTCTCCCGGGCTGAGGTC 180
Db 121 CCGCTGTCTACTGCTCTGATGGCTTCGTGAGCTTCGTGAGCTTCCTCCCGGGCTGAGGTC 180
QY 181 ATGAGCGGGGCTGTGCTCTCTCTCTTTATGGGCCAGACACAGTAGTGAGCTGCTCCG 240
Db 181 ATGAGCGGGGCTGTGCTCTCTCTCTTTATGGGCCAGACACAGTAGTGAGCTGCTCCG 240
QY 241 CACAGATCCGAGGCGCTGGAGGACCAAGAGTTCAAGGCTGAGCTGATCCCTGTAC 300
Db 241 CACAGATCCGAGGCGCTGGAGGACCAAGAGTTCAAGGCTGAGCTGATCCCTGTAC 300
QY 301 CGGAAGAGCGGGCTCCCGTCTCTGATGTGATGATGATGATGATGATGATGATGATGAT 360
Db 301 CGGAAGAGCGGGCTCCCGTCTCTGATGTGATGATGATGATGATGATGATGATGATGAT 360
QY 361 GGGGAGTGGCT 420
Db 361 GGGGAGTGGCT 420
QY 421 GGGCCCGACAGATCAAGAGGACAGGTGGTGGCGCGCGCGATGATGCGCGGACAGTCC 480
Db 421 GGGCCCGACAGATCAAGAGGACAGGTGGTGGCGCGCGCGATGATGCGCGGACAGTCC 480
QY 481 AAAGGCTTCAATGCG 540
Db 481 AAAGGCTTCAATGCG 540
QY 541 CTGCAGAGGAGCGCCCAAGGCGCAAGCAAGCTCAATAGGGGTGTGTGGGAGAGAACCA 600
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QY 601 AACTTGCTGAGTACAAAGTAGCGCCATCGGAAAGTGGCGCTTCATCTCTCTCTCTCTCT 660
Db 601 AACTTGCTGAGTACAAAGTAGCGCCATCGGAAAGTGGCGCTTCATCTCTCTCTCTCTCT 660
QY 661 GGGGACTGAGACCCCTGGGATGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
Db 661 GGGGACTGAGACCCCTGGGATGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
QY 721 ACTGTGCTTACAGCGTGTGTGTGAGCAGCAGCGGAGCGCGCGCGCGCGCGCGCGCGCG 780
Db 721 ACTGTGCTTACAGCGTGTGTGTGAGCAGCAGCGGAGCGCGCGCGCGCGCGCGCGCGCG 780
QY 781 CCCAGGCTGTGAGCTGGCGCGTGGAGGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
Db 781 CCCAGGCTGTGAGCTGGCGCGTGGAGGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
QY 841 CGTACCACATTCGTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 841 CGTACCACATTCGTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 901 CACTACGTCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 901 CACTACGTCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 CATGCCCTCAAGGTCAACGTGTACTTCGGGGCCCATCTGCTGAAGAGCGGTGCGCCTGCTG 1020
Db 961 CATGCCCTCAAGGTCAACGTGTACTTCGGGGCCCATCTGCTGAAGAGCGGTGCGCCTGCTG 1020

QY	1021	CGCCTGCTGGCCCTGCTTCCGCGCGCTGGACCGGTACTCGCAGTACAGCGCCGCTGGTGCTTG	1080
DB	1021	CGCCTGCTGGCCCTGCTTCCGCGCGCTGGACCGGTACTCGCAGTACAGCGCCGCTGGTGCTTG	1080
QY	1081	ACACTGCTCATGCCGTGTTGCCCTGCTCGGCACCTGGGTCCGCTCGCTGCTGCTGTTTAC	1140
DB	1081	ACACTGCTCATGCCGTGTTGCCCTGCTTGGCCTGTGGCAGTGGTTGCCCTGCTGCTGTTTAC	1140
QY	1141	ATTGGCCAGCGGAGATCGAGAGACGCGAATCGAGCTGCCITGAGATTGGCTGGCTGCGAG	1200
DB	1141	ATTGGTCAGCGGAGATCGAGAGACGCGAATCGAGCTGGCTCGAGATTGGCTGGCTGCGAG	1200
QY	1201	GAGCTGGCCCGCCGACTGGAGACTCCCTACTACTCTGCTGCTGGCCGCGAGCCAGCTGGAGGG	1260
DB	1201	GAGCTGGCCCGCCGACTGGAGACCCCTACTACTTGGTGGCCCGAGAGACCGCCGAGGGG	1260
QY	1261	AACAGCTCCGGCCAGAGTGACAACTCGACAGCAGCAGCAGGAGGCCAACGGAGCGGCGTG	1320
DB	1261	AACAGCTCTGGCCAGAGTGACAACTCGACAGCAGCAGCAGGAGGCCAACGGAGCGGCGTG	1320
QY	1321	GAGCTGCTGGCGGCCGCTCGCTGGCGAGCGCCTACATCACTTCCCTCTACTTCTGCACTC	1380
DB	1321	GAGCTGCTAGCGGCCGCTCGCTGGCGAGCGCCTACATCACTTCCCTCTACTTCTGCACTC	1380
QY	1381	AGCAGCCTACCAAGCGTGGCCTTCGGCAAGCTGTCCGCCAACGACGACACCGAGAGATC	1440
DB	1381	AGCAGCCTACCAAGCGTGGCCTTCGGCAACGCTGTCCGCCAACGAGACTGAGAAGATC	1440
QY	1441	TTCTCCATCTGCACCATGCTCATCGGGCGCCCTGATGCACGCGTGGTGTTCGGGAGCTG	1500
DB	1441	TTCTCCATCTGCACCATGCTCATCGGGCGCCCTGATGCACGCGTGGTGTTCGGGAGCTG	1500
QY	1501	ACGGCCATCATCAGCGCATGTACGCCCGCGCTTCTGTACCAACAGCCGACGCGCGGAC	1560
DB	1501	ACGGCCATCATCAGCGCATGTACGCCCGCGCTTCTGTACCAACAGCCGACGCGCGGAC	1560
QY	1561	CTGGCGACTACATCGCATCCACCGTATCCCAAGCCCTCTCAAGCAGCCGATGCTGGAG	1620
DB	1561	CTGGCGACTACATCCGCATCCACCGTATCCCAAGCCCTCTCAAGCAGCCGATGCTGGAG	1620
QY	1621	TACTTCCAGCCACTCGGCGGTGAACAATGGATCGACACCAACCGAGCTGCTGCAGAGC	1680
DB	1621	TACTTCCAGCCACTCGGCGGTGAACAATGGATCGACACCAACCGAGCTGCTGCAGAGC	1680
QY	1681	CTCCTGCAGAGCTGCGCGCAGACATCGCCATGCACCTGCACAAGAGGTCTCTGCAGCTG	1740
DB	1681	CTCCTGCAGAGCTGCGCGCAGACATCGCCATGCACCTGCACAAGAGAGTCTCTGCAGCTG	1740
QY	1741	CCACTGTTTGAGCGGCCAGCCCGGTGCTCGGGCACTGTCTCTGGCCCTCGCGGCC	1800
DB	1741	CCGCTGTTTGAGGCAGCAGCCGGGTGCTCGGGGCACTGTCTCTGGCCCTCGCGGCC	1800
QY	1801	GCCTTCTGCAGCGCGCGGAGTACTCATCAACCAAGCGATGCCCTGCAGGCGCCTCTAC	1860
DB	1801	GCCTTCTGCAGCGCGCGGAGTACTCATCAACCAAGCGATGCCCTGCAGGCGCCTCTAC	1860
QY	1861	TTTGCTGCTCTGCTCCATGGAGGTGCTCAAGGGTGGCAGCTGCTCGCCATCTCTAGGG	1920
DB	1861	TTTGCTGCTCTGCTCCATGGAGGTGCTCAAGGGTGGCAGCTGCTCGCCATCTCTAGGG	1920
QY	1921	AAGGGCCACTGTACGCTGTGACTGCCCGGGGAGCAGGTGGTAAAGGCCAATGCC	1980
DB	1921	AAGGGTGACTGTACGCTGTGACTGCCCGGAGCAGCAGGTGGTAAAGGCCAAGGCC	1980
QY	1981	GAGCTGAAGGGGCTGACGTACTCGGTCTCGAGTGTCTGACGTGGCTGGCTCTCAGGAC	2040
DB	1981	GATGTGAAGGGGCTGACGTACTCGGTCTCGAGTGTCTGACGTGGCTGGCTCTCAGGAC	2040
QY	2041	AGCCTTCGCGTGTACCCCGAGTTTGGCCCGCGCTTTCAGTGTGGCTTCCGAGGGGAGCTC	2100
DB	2041	AGCCTTCGCGTGTACCCCGAGTTTGGCCCGCGCTTTCAGTGTGGCTTCCGAGGGGAGCTC	2100
QY	2101	AGCTACAACTGGTGTGGGGAGGCTCTGCAGAGGTGGACACCACTGCTCTGAGCGG	2160

[illegible]

Db 3181 GAGATGGTCTATTGCTTCCACGGCTCTGGACACTCCAGTCGAGTGGACCCAGGAAGAGC 3340
QY 3241 ACAGGGTTC 3249
Db 3241 ACAGGGTTC 3249
RESULT 7
US-09-119-855-3
: Sequence 3, Application US/09119855
: Patent No. US20020099197A1
: GENERAL INFORMATION:
: APPLICANT: Curtis, Roy A. J.
: TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
: FILE REFERENCE: mnl-055
: CURRENT APPLICATION NUMBER: US/09/119.855
: CURRENT FILING DATE: 1998-07-21
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: PatentIn ver. 2.0
: SEQ ID NO 3
: LENGTH: 3240
: TYPE: DNA
: ORGANISM: Monkey
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(3240)
US-09-119-855-3
Query Match 96.7%; Score 3144; DB 9; Length 3240;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 3180; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
QY 10 ATGGGGGCTCTGGGGCTTCAGAACACCTTCTGGACACCATCGGTACGGCTTCGAC 69
Db 1 ATGGGGGCTCTCTGGGGCTTCAGAACACCTTCTGGACACCATCGGTACGGCTTCGAC 60
QY 70 GGCACGCACACTTCTGGCTGGGCAACGCCAGCTGGCGGGCTCTTCGGGTGGTC 129
Db 61 GGCACGCACACTTCTGGCTGGGCAACGCCAGCTGGCGGGCTCTTCGGGTGGTC 120
QY 130 TACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTATGACAGCG 189
Db 121 TACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTATGACAGCG 180
QY 190 GGCTGTGCTCTCTCTCTTTATGGGCCAGACACAGTGTGAGCTGTCCGCCAACAGATC 249
Db 181 GGCTGTGCTCTCTCTCTTTATGGGCCAGACACAGTGTGAGCTGTCCGCCAACAGATC 240
QY 250 CGAAGGCCCTGGAGCAGACACAGGTTCAAGGCTGAGCTGATCTCTGTACCGGAAGAGC 309
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QY 310 GGGTCTCCGTTCTGTGTCTCTCTGGAATCAAGGCTGAGCTGATCTCTGTACCGGAAGAGC 369
Db 301 GGGTCTCCGTTCTGTGTCTCTCTGGAATCAAGGCTGAGCTGATCTCTGTACCGGAAGAGC 360
QY 370 GCTCTCTCTCTAGTCTCTCAAGSAGATCAGCGAAACACAGACCGAGCGGCCCGAC 429
Db 361 GCTCTCTCTCTAGTCTCTCAAGSAGATCAGTGAACCAAGACCGAGCGGCCCGAC 420
QY 430 AGATGGAGGAGACAGGTGTGGCGGCGCGGATATGGCGGGGACCATCCAAAGGCTTC 459
Db 421 AGATGGAGGAGACAGGTGTGGCGGCGCGGATATGGCGGGGACCATCCAAAGGCTTC 450
QY 490 AATGCCAACCGGGCGGAGCGCGGCGTGTCTTACCACCTGTCCGGGACCTTCGAGAAG 549
Db 481 AATGCCAACCGGGCGGAGCGCGGCGTGTCTTACCACCTGTCCGGGACCTTCGAGAAG 540
QY 550 CAGCCCAAGGCGACACAACTCAATAAGGGGTGTCTGGGAGAACCAACTTCGCT 609
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Db 601 GAGTACAAAGTAGTCCCATCGGAAGTCGCCCTTCACTCTGTTGCATCTGTGGGCGCTG 660
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Db 841 TTTGCTGTCCAGTCCGGGCGGAGTGTGTGTGTGTGTTGCCCAAGTGCATTTGCTCCATAGCTC 900
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Db 901 ACCAGCTGGTTCCTGCTGATGTGATCGACGGTGGCTTGTGACCTGCTACATGCCCTTC 960
QY 970 AAGTCAAGGTGTATTTCCGGGCCCATCTGTGTGAAGCGGTGCGGCTGCTCGGCTGCTG 1029
Db 961 AAGTCAAGGTGTATTTCCGGGCCCATCTGTGTGAAGCGGTGCGGCTGCTCGGCTGCTG 1020
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QY 1570 TACATCCGATCCACCGTATCCCCAAGCCCTCAAGCAGCGCATGCTGGAGTACTTCCAG 1629
Db 1561 TACATCCGATCCACCGTATCCCCAAGCCCTCAAGCAGCGCATGCTGGAGTACTTCCAG 1620
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Db 1621 GCCACTGGGGGTGAACAATGGCATCCAGACACCGAGCTGCTGCAGAGCCTCCCTGAC 1680
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Db 1741 GAGCAGCAGCCCGGGCTGGCTCGGGCACTGTCTGTGGCCCTGGCGCCGCGCTTTCG 1808
Qy 1810 ACGCGGGCGAGTAGCTCATCCACCAAGAGGATGCCCTGCAGGCGCTCTACTTTGTCTGC 1869
Db 1801 ACGCGGGCGAGTAGCTCATCCACCAAGGCGATGCCCTGCAGGCGCTCTACTTTGTCTGC 1860
Qy 1870 TCTGGCTCCATGAGAGTGTCTCAAGGTGGCACTGTGTGGCCATCTCTAGGAAGGGGAC 1929
Db 1861 TCTGGCTCCATGAGAGTGTCTCAAGGTGGCACTGTGTGGCCATCTCTAGGAAGGGGAC 1920
Qy 1930 CTGATCGGCTGTAGCTGCCCGGGGAGAGAGTGGTAAAGGCCAATGCCAGCIGAG 1989
Db 1921 CTGATCGGCTGTAGCTGCCCGGGGAGAGAGTGGTAAAGGCCAATGCCAGTGTGAG 1980
Qy 1990 GGGCTGAGCTACTGCGTCTCTGACGTGTCTGACGTGGCTGGCTGSCACGACAGCTTTCG 2049
Db 1981 GGGCTGAGC:ACTGCGTCTGCACTGTCTGACGTGGCTGGCTGSCACGACAGCTTTCG 2040
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Db 2041 CTTACCCCGAGTTTGGCCCGCTTCCAGTGTGTGAGTGGCTGGCTGSCAGGAGCTCAGCTACAC 2100
Qy 2110 CTGGGTGCTGGGGAGGCTCTGCAGAGTGGACACAGCTCCCTGAGGGGAGCAATACG 2159
Db 2101 CTGGGTGCTGGGGAGGCTCTGCAGAGTGGACACAGCTCCCTGAGGGGAGCAATACG 2150
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Db 2161 CTTATGTCCACGCTGGAGGAGAGGACAGATGGGAGCAGGCGCCCAAGTCTCCCA 2220
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Db 2221 GCCCAGCTGATGAGCCCTCAGGCGCCCTGCTGTGGCTGGCTGSCACTCTCATCTCA 2280
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Qy 2410 CTAGAGGGCTACGGCTGCCCGCCATGCCATGGATGTGCCCGCAGATCTAGCCGAG 2469
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Qy 2470 GTAGTAGATGGCATTTGAGAGCGGCTGTGGCTCGGACACGCGCAAGTCTCTTCCGGGTG 2529
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Db 2521 GGCAGTGTGCCCGGAATGTAGCAGCAGCCCTTCCCTGACACGAGAGTGTGGCTCTC 2580
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Qy 2650 GCGGTGACAGAGCTGTACAGAGCGGTGTCCAGATGCCGAGGAGGACTGCAGTCACTTCG 2709
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Qy 2830 GCATCTCTACTGCTGCAGCCCGCAGCTGGCTGTGTGTGAGTGGAGCTTGGCCCCAC 2889
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Qy 2950 AGTCCGCTGGCTCGAGGCGACAGTTTCTGACCTCCACCTCAGACTCAGAGCCCCCT 3009
Db 2941 AGTCCGCTGGCTCGAGGCGACAGTTTCTGACCTCCACCTCAGACTCAGAGCCCCCT 3000
Qy 3010 GCTCAGGAGACCTCTGCTGAGCGCAGCAGCCCTGCCCTCCCTCTCTCTCTGAGGAA 3069
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Qy 3070 GGGCTAGGACTGGGCGCGCAGACCTGTGAGCGCAGGCTGAGGCTACACAGCTGAGAG 3129
Db 3061 GGGCTAGGACTGGGCGCGCAGACCTGTGAGCGCAGGCTGAGGCTACACAGCTGAGAG 3120
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Db 3121 CCCCAGCAGTGTACAGGGGCGCTGGCTTGGCTTGGAGCCCGCAGCCCTGGAGATGCTC 3180
Qy 3190 CTTATTGGCTGCCATGGCTCTGGCAGAGTCCAGTGGACCCAGCAAGACAGCGGGTC 3249
Db 3181 CTTATTGGCTGCCAGGCTCTGGCAGAGTCCAGTGGACCCAGCAAGACAGCGGGTC 3240

RESULT #
US-9-965-830-9
; Sequence 9, Application US/09965830
; Patent No. US20020177201A1
; GENERAL INFORMATION:
; APPLICANT: Iyanouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: A novel potassium channel protein
; FILE REFERENCE: Y9903-PC1
; CURRENT APPLICATION NUMBER: US/09/965,830
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 09/600,776
; PRIOR FILING DATE: 2001-07-21
; PRIOR APPLICATION NUMBER: JP P1998-346198
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-965-830-9

Query Match 81.9% Score 2664.8; DB 10; Length 3715;
Best Local Similarity 89.0% Pred. No. 0;
Matches 2905; Conservative 0; Mismatches 347; Indels 12; Gaps 2;
Qy 1 ATGCGGCCCATGGGGGCTCTCTGGCGCCCTCAGAACACCTTCTCTGGACACCATCGCTACG 60
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Qy 61 CGTTTCAGCGGCGACGACAGTAACCTTCTGCTGGGCAACGCCAGGTGGGGGCTCTTTC 120
Db 216 CGTTTCAGCGGCGACGACAGTAACCTTCTGCTGGGCAACGCCAGGTGGCGGCTCTTTC 275
Qy 121 CCGTGTGCTACTGCTCTGTATGGCTTCTGTGACCTCAGCGGCTTCTCCGGGCTGAGGTC 180
Db 276 CCGTGTGCTACTGCTCTCCGATGGCTTCTGTGACCTCAGCGGTTTCTCCAGAGCTGAGGTC 335
Qy 181 ATCAGCGGGGCTGTGCTCTCTCTCTCTTATGGCGCAGACACCATGAGTGCCTGCTCCGC 240
Db 336 ATCAGCGAGGCTGTGCCTGCTCTCTCTCTATGGCGCAGACACCATGAGTGTGCTCCGC 395
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[illegible]

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1536	TTGGCGCTCAGCACTCTCACCAGTGTGGGCTTCGGCAATGTGTCCGCTACACAGACACT	1595
1432	GAGAAGATCTTCTCCATCTGCACCATGCTCATCGGGCCCTGTATGCACGGTGGTGT	1491
1596	GAGAAGATTTCCTCCATCTGCACCATGCTTAITGGAGCTCTGATGATCAGTGTGT	1655
1492	GGGAACGTCAGCGCCATCATCCAGCGCATGTAGCCCGCCGCTTCTGTACACAGCGGC	1551
1656	GGGAATTTGACAGCCATCAFCACAGCCATGTACGTGCGGCGTTCTGTGTACACAGCGGC	1715
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1716	ACCGTGAACCTGGAGACTACATTCGCATCCACGGCATCCCAAGGCCCTCAACAGCGC	1775
1612	ATGCTGGAGTACTCCAGGCCACCTGGGCGGTGAACAAATGGCATCGACACACCGAGCTG	1671
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1672	CTGCAGAGCTCCCTGACGAGCTGCAGCAGACATCGCCATGCACCTGCACAGGAGTCT	1731
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1852	GGCCTCTACTTTGCTGCTCTGCTCATCGAGGTGCTCAAGGTGCACGGTGCCTGCC	1911
2016	GCCTCTACTTTGCTGCTCAGGTTCCATGGAGTCTCTCAAGGTGCACGGTGCCTGCC	2075
1912	ATCCTAGGAAGGGCACCTGATCGGCTGTGAGCTGCCCGCGGGAGCAGGTGGTAAG	1971
2076	ATTCTAGGAAGGTTGACCTGATCGGCTGTGAGCTGCCCGCGGGAGCAGGTGGTAAG	2135
1972	GCCAATGCGACGTGAAGGGCTGACGATACCTGGCTCTGAGCTGTGCAAGCTGGCTGGC	2031
2136	GCCAATGCGACGTGAAGGGCTGACATACCTGGCTCTGAGCTGTGCAAGCTGGCTGGC	2195
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2196	CTGCAGCAGCCCTGGGCTGACCCGAGCTTGCCTGGCTCTGAGCTGTGCAAGCTGGCTGGC	2255
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2256	GGGAGCTCAGCTACAACTGGGCTGGAGGAGTGTCTGCAGAGGTGGATACCACTCA	2315
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2316	CTGAGTGGTGACAAACCCCTCATCTCCACTGGAGGAGGAGACAGATGGGAGCAA	2375
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2376	GGACACAGCATCTCACGAGCCCGCAGAGATGAGCCCTCCAGCCCGCTGTCTCACCTGGC	2435
2272	TGCACCTCTCATCTCAGCTGCGCAAGCTCTATCCCGACGTGCAACAGCACCCCGGCT	2331
2436	TGTACCTCTCTCTCAGGGGCGCAACTACTCTCCCGAGCTGCACTGACCCCGGCGC	2495
2332	CGTCTAGTGTGCGAGGGAGCGCAGCGGAGGGGCTTTGAAGGCTGAGGCTGGCCCGC	2391
2496	AGGCTGGTGGCAGAGGGGGCCCACTAGGGCAGGGGTTTGAAGCCTGAGGCTGGTCT	2555
2392	CTGTCTCCCGCAGGCGCCTAGAGGGCTACGGCTGCCCGCCCATGCCATGCCATGTGCC	2451
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QY 2512 AAGTTCTCTTCCCGCTGGGCGAGCTGCGCCGGAATGTAGCAGCAGCCCTCCCTCGGA 2571
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QY 2812 CTGTGTGTGACACTGGGGCATCCTCTCTACTGTGCTGCTGACGCGCCGAGCTGCTGTG 2871
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RESULT 9

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; Sequence 5, Application US/09965830
; Patent No. US20020177201A1
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: A novel potassium channel protein
; FILE REFERENCE: Y9903-PCT
; CURRENT APPLICATION NUMBER: US/09/965.830
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 09/600, 776
; PRIOR FILING DATE: 2001-07-21
; PRIOR APPLICATION NUMBER: JP P1998-346198
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 12
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; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5

; LENGTH: 3064

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (4)..(3057)

US-09-965-830-5

Query Match

Best Local Similarity 27.2%; Score 884.8; DB 10; Length 3064;

Matches 1408; Conservative 0; Mismatches 622; Indels 120; Gaps 3;

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QY 301 CGGAAGAGCGGCTCCGCTTCTGCTGCTGCTGATGATACCCATGAAGATGAGAA 360
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Qy 1963 -----GTGTAAGGCCAATGCCGACGTGAAGGGGCTGACGTACTTGGCTC 2007
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Qy 2008 CTGCAGTGTCTGCACTGGCTGCGCTGCACGACAGCCCTGCGCTGTACCCGAGTTTGGCC 2067
Db 2092 CTGCAGCAGCTGAGCAGCGGAGGCTGCGCGAGGCTCTGCGTGTATCCGGAATATGT 2151
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RESULT 11
US-09-119-855-9
: Sequence 9, Application US/09119855
: Patent No. US20020099197A1
: GENERAL INFORMATION:
: APPLICANT: Curtis, Rory A.J.
: TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
: FILE REFERENCE: mai-055
: CURRENT APPLICATION NUMBER: US/09/119,855
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 9
: LENGTH: 870
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(870)
US-09-119-855-9

Query Match 26.08; Score 844.4; DB 9; Length 870;
Best Local Similarity 99.9%; Pred. No. 3.8e-200;
Matches 845; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCGCGCCATGCGGGCCCTCCCTGGCGCCTCAGAACACCTTCTCTGGACACCATCGCTACG 60
Db 1 ATGCGCGCCATGCGGGCCCTCCCTGGCGCCTCAGAACACCTTCTCTGGACACCATCGCTACG 60
Qy 61 CGCTTCAGCGCAGCAGCACTTAAGTTCGTGTGGCAACGCCAGGTGGCGGGCTCTTC 120
Db 61 CGCTTCAGCGCAGCAGCACTTAAGTTCGTGTGGCAACGCCAGGTGGCGGGCTCTTC 120
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Qy 301 CGGAAGAGCGGCTGCT 360
Db 301 CGGAAGAGCGGCTGCT 360
Qy 361 GGGAGGTGGCT 420
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Qy 541 CTGAGAGCGGCTGCT 600
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RESULT 12
US-10-185-867-9
; Sequence 9, Application US/20185867
; Publication No. US20030104429A1
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/10/185,667
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US/09/358,383
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: US/09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

LOCATION: (1)-(870)
US-10-185-867-9
Query Match 26.0%; Score 844.4; DB 14; Length 870;
Best Local Similarity 99.9%; Pred. No. 3.8e-200;
Matches 845; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 541 CTGAGAGCGGCTGCT 600
Db 541 CTGAGAGCGGCTGCT 600
Qy 601 AACTTGCTGAGTCAAGTACCGGCTTCAATGAGGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
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Qy 781 CCCAGCTGTGACCTGGCGGCT 840
Db 781 CCCAGCTGTGACCTGGCGGCT 840
Qy 841 CGTACC 846
Db 841 CGTACC 846

RESULT 13
US-09-119-855-7
; Sequence 7, Application US/09119855
; Patent No. US2002009197A1
; GENERAL INFORMATION:

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; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: mni-055
; CURRENT APPLICATION NUMBER: US/09/119,855
; CURRENT FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (263)..(1132)
US-09-119-855-7

Query Match      26.0%; Score 844.4; DB 9; Length 1132;
Best Local Similarity 99.9%; Pred. No. 4e-200;
Matches 845; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCGGCCATGCGGGGCTCTCTGGCGCTCAGAACACCTTCTCTGGACACCATCGCTACG 60
DB 263 ATGCGGCCATGCGGGGCTCTCTGGCGCGCAGAACACCTTCTCTGGACACCATCGCTACG 322
QY 61 CGCTTCACGCCACGACAGTAACITCGTGGGCAACGCCAGGTGGCGGGCTCTTC 120
DB 323 CGCTTCACGCCACGACAGTAACITCGTGGGCAACGCCAGGTGGCGGGCTCTTC 382
QY 121 CCCGTGCTACTGCTCTGATGGCTTCTGTGACCTCAGCGGCTTCTCCGGGGTGGAGTC 180
DB 383 CCCGTGCTACTGCTCTGATGGCTTCTGTGACCTCAGCGGCTTCTCCGGGGTGGAGTC 442
QY 181 ATGCGAGGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 443 ATGCGAGGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 241 CAACAGATCGCAAGGCCCTGGACGACACAGAGTCAAGGCTGAGCTGATCTCTATC 300
DB 503 CAACAGATCGCAAGGCCCTGGACGACACAGAGTCAAGGCTGAGCTGATCTCTATC 562
QY 301 CGGAGAGCGCCCAAGGCGCAAGCAAGCTCAATAAGGGGGTGTGGGAGAAACCA 600
DB 803 CTGCAAGAGCGCCCAAGGCGCAAGCAAGCTCAATAAGGGGGTGTGGGAGAAACCA 862
QY 601 AACTTGCTGAGTCAAAAGTACCGCCCATCGGGAAGTCGGCCCTCATCTCTGTCAC 660
DB 863 AACTTGCTGAGTCAAAAGTACCGCCCATCGGGAAGTCGGCCCTCATCTCTGTCAC 922
QY 661 GGGCACTGAGAGCACTGGGATGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
DB 923 GGGCACTGAGAGCACTGGGATGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 982
QY 721 ACTGTGCCCTACAGCGTGTGTGTGAGCACAGCAGCGGAGGCCAGTGGCGCGCGGCGG 780
DB 983 ACTGTGCCCTACAGCGTGTGTGTGAGCACAGCAGCGGAGGCCAGTGGCGCGCGGCGG 1042
QY 781 CCCAGCGTCTGTGACCTGGCGGTGGAGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
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DB 1043 CCACAGCGTGTGACCTGGCGGTGGAGTCTCTCTCATCTTGACATTTGCTGAATTC 1102
QY 841 CGTACC 846
DB 1103 CGTACC 1108

RESULT 14
US-10-185-867-7
; Sequence 7, Application US/10185867
; Publication No. US20030104429A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; CURRENT APPLICATION NUMBER: US/10/185,867
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US/09/358,383
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USSN 09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (263)..(1132)
US-10-185-867-7

Query Match      26.0%; Score 844.4; DB 14; Length 1132;
Best Local Similarity 99.9%; Pred. No. 4e-200;
Matches 845; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCGGCCATGCGGGGCTCTCTGGCGCTCAGAACACCTTCTCTGGACACCATCGCTACG 60
DB 263 ATGCGGCCATGCGGGGCTCTCTGGCGCGCAGAACACCTTCTCTGGACACCATCGCTACG 322
QY 61 CGCTTCACGCCACGACAGTAACITCGTGGGCAACGCCAGGTGGCGGGCTCTTC 120
DB 323 CGCTTCACGCCACGACAGTAACITCGTGGGCAACGCCAGGTGGCGGGCTCTTC 382
QY 121 CCCGTGCTACTGCTCTGATGGCTTCTGTGACCTCAGCGGCTTCTCCGGGGTGGAGTC 180
DB 383 CCCGTGCTACTGCTCTGATGGCTTCTGTGACCTCAGCGGCTTCTCCGGGGTGGAGTC 442
QY 181 ATGCGAGGGGCTGTGCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
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DB 623 GGGAGAGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 682
QY 421 GGGCCCGACAGATGGAAGAGAGACAGGTGGTGGCGCGCGCGCGCGCGCGCGCGCG 480
DB 683 GGGCCCGACAGATGGAAGAGAGACAGGTGGTGGCGCGCGCGCGCGCGCGCGCGCG 742
QY 481 AAAGGCTTCAATGCCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
DB 743 AAAGGCTTCAATGCCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 802
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 DB 863 AACTTGCCTGAGTACAAAGTAGCCGCCATCGGGAAGTGGCCCTTCATCTGTCAGTGT 922
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 QY 781 CCCAGGCTGTGACTGGCCGTGGAGGTCTCTTCATCTGCTGACTGTGCTGAAATTC 840
 DB 1043 CCCAGGCTGTGACTGGCCGTGGAGGTCTCTTCATCTGCTGACTGTGCTGAAATTC 1102
 QY 841 CGTACC 846
 DB 1103 CGTACC 1108

RESULT 15
 US-10-185-867-17
 ; Sequence 17, Application US/10185867
 ; Publication No. US20030104429A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Curtis, Hory A.J.
 ; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
 ; FILE REFERENCE: MNI-055CP
 ; CURRENT APPLICATION NUMBER: US/10/185,867
 ; CURRENT FILING DATE: 2002-06-27
 ; PRIOR APPLICATION NUMBER: US/09/358,383
 ; PRIOR FILING DATE: 1999-07-21
 ; PRIOR APPLICATION NUMBER: USN 09/119,855
 ; PRIOR FILING DATE: 1998-07-21
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 17
 ; LENGTH: 3321
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(3321)
 US-10-185-867-17

Query Match 23.4%; Score 761.2; DB 14; Length 3321;
 Best Local Similarity 62.2%; Pred. No. 2,2e-179;
 Matches 1319; Conservative 0; Mismatches 708; Indels 93; Gaps 4;

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 DB 61 CGTTTTCGAGCAACATAGCAACATCATCTTGGCAATGCCAGGTGGCTAAGGTTC 120
 QY 121 CCGGTGCTACTGCTCTGATGGCTTCTGTGACCTACAGGGTTCCTCCGGGCTGAGTC 180
 DB 121 CCCATAGTCTACTGTTCCGAGTCTCTGCGAGTCTGTGGATTTGCCCGAACTGAAGTC 180
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 DB 181 ATGCAAGAGTGTGAGTCTGAGTCTTATTTGGGTTGAAACCAATGAGCAACTGATG 240
 QY 241 CAACAGATCGGAAGGCTTGGACGACGACAGAGGTTCAGAGGCTGAGCTGATCTGTAC 300
 DB 241 CTTCAATAGAAAGTCACTGGAGGAGAAACAGATTCAGAGGAGAAATATATGTTAC 300

QY 301 CSGAAGACGGGCTCCGCTTCTGCTCTGATGTGATACCCATAAAGATGAGAA 360
 DB 301 AAGAAAACGGGCTCTCAATTTGGTGGCTACTGGATATTTGTTCCCAATAAGAAATGAAAA 360
 QY 361 GGGAGGTGGCTCTCTTCCCTAGTCTCTCAAGAGCATCAGGAAACCAACCAAGGAG 420
 DB 361 GGAGATGATGATCTTTTCTGGCTCTGTTCAAGATATAACAGATA-CAAAAGTGAAGAT 419
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 DB 477 -----CTTTCAGCTCAGCCGCGAGCGAGTCTGCTTATCACATCTCTGGGAC 531
 QY 541 CTGAGAGCAGCCCAAGGCAAGCAGCAGCTCAATAGGGGCTGTTGGGAGAAACCA 600
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 QY 601 AACTTGCTGAGTACAAAGTAGCGGCATCCGGAAGTCGCCCTTCATCTGTGCACTGT 660
 DB 592 GCATTTCCGGAGTATAAGTTTCTGATGCAAAAAGTCCAAATTCATCTCTGCATTTT 651
 QY 661 GGGCACTGAGAGCCACTGGGATGGCTTCATCTGCTGCCACACTCTAIGTGGCTGT 720
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 DB 712 ACTGTACTTACACGTTTGTCTTATTTGGCAATGAGCAGCTGCCAATCTCGGAG- 768
 QY 781 CCCAGCTGTGACCTGGCGGTGGAGTCTCTTCATCTGACATTTGCTGCAATTC 840
 DB 769 ARAACCTGAGTGCATTCAGTGGAGATCTTTTATATAGATATATTTAAATTC 828
 QY 841 CGTACACATCTGTGCTCAAGTGGGCGGAGTGGTGTTCGCCCAAGTCCATTTGCTC 900
 DB 829 CGAAACACTTATGTGACAGAGTGTGGCAAGTATCTTTGAAGCAGATCAATTTGCATC 886
 QY 901 CACTACCTACCACTGTTCTGCTGATGTATCGAGCGCTGCGCTTTCAGCTGCTA 960
 DB 889 CACTATGTCAACACTGTTCTATCATTTAATCGCTGCCCTTTCCTTTGATCTTCG 948
 QY 961 CATGCTTCAAGTCAACAGTGTACTTGGGCGCCATCTGCTGAAGAGCGTGGCGCTG 1020
 DB 949 TATGCTTTCAAGCTCACAGTGGTGTCTCTGTCATCTCTAAAGACAGTGGCGCTTG 1008
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 QY 1201 GAGTGGCGCGCGCTGAGACTCCCTACTACTGTTGGCGGAGGCGGCGGAGG 1260
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 QY 1261 AACAGCTCGGCCAGATGACAACTGCGAGCAGCAGCAGGCAACGAGCGGCGCTG 1320
 DB 1222 -----GCAAC 1227
 QY 1321 GAGTGTGGCGCGCGCTGCTGCGAGGCGCTTACATCACTCCCTCTACTTCGCACTC 1380
 DB 1228 AATACCTTGGGGCGCGCTCGATCCGAAGTGCCTATATTGCGGCTCTGTACTTCACGCTG 1287

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2003, 15:33:20 : Search time 5966 Seconds
(without alignments)
13248.095 Million cell updates/sec

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Perfect score: 3252

Sequence: 1 atgcgcgcacatgcgggcct.....aagaagccacaggggtctga 3252

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_est6:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_fod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gssi:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	802.4	24.7	896	12	BM452074	BM452074	BM452074 AGENCOURT
3	783.4	24.1	4015	11	AK048629	AK048629	AK048629 Mus muscu
4	675.6	20.8	862	13	BU187340	BU187340	BU187340 AGENCOURT

5	662.8	20.4	766	10	BE795800	BE795800	BE795800 601590834
6	658.4	20.2	714	10	BE778330	BE778330	BE778330 601463723
7	608.6	18.7	617	9	AW249035	AW249035	AW249035 2820908.5
8	582.4	17.9	704	14	CD354565	CD354565	CD354565 U1-M-GMO-
9	550.6	16.9	651	9	AL134774	AL134774	AL134774 DKEPDP5471
10	492	15.1	501	9	AW249298	AW249298	AW249298 2821074.5
11	477	14.7	865	14	CD106245	CD106245	CD106245 AGENCOURT
12	470	14.5	482	10	BE266788	BE266788	BE266788 601190462
13	424	13.0	424	9	A1272282	A1272282	A1272282 ap23c04.x
14	369.8	11.4	682	13	BQ444229	BQ444229	BQ444229 U1-M-EXO-
15	361	11.1	522	12	BI975332	BI975332	BI975332 483675 MA
16	345	10.6	710	12	BQ045257	BQ045257	BQ045257 U1-CF-EN1
17	337.4	10.4	387	14	R35526	R35526	R35526 Y964e08.r1
18	335.2	10.3	502	10	EG082483	EG082483	EG082483 H3076F11-
19	328.4	10.1	463	14	R73353	R73353	R73353 Y10e04.r1
20	315.6	9.7	572	14	CB055396	CB055396	CB055396 NISC-J103
21	313	9.6	391	14	R13511	R13511	R13511 Yf59c02.r1
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23	305.6	9.4	328	9	AA325048	AA325048	AA325048 EST27376
24	305	9.4	717	10	EG089378	EG089378	EG089378 H3076F11-
25	301.4	9.3	1076	12	BM561167	BM561167	BM561167 AGENCOURT
26	294.4	9.1	1115	12	BM547060	BM547060	BM547060 AGENCOURT
27	284.2	8.7	351	14	R35105	R35105	R35105 Yg59f09.r1
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29	271.4	8.3	438	14	CB751495	CB751495	CB751495 AMGNNUC.N
30	261.8	8.1	337	10	BF449484	BF449484	BF449484 maa43d03
31	259.8	8.0	909	13	BX391570	BX391570	BX391570 BX391570
32	256.8	8.0	924	14	CA454037	CA454037	CA454037 AGENCOURT
33	256	7.9	878	13	BU170580	BU170580	BU170580 AGENCOURT
34	255.8	7.9	615	14	CB579755	CB579755	CB579755 AMGNNUC.N
35	246.6	7.6	635	10	BF589083	BF589083	BF589083 oac28c08
36	246	7.6	661	12	BI390873	BI390873	BI390873 p9plp.pk2
37	242.8	7.5	4059	11	AK042438	AK042438	AK042438 Mus muscu
38	242.2	7.4	749	13	BU0707188	BU0707188	BU0707188 U1-M-FRO-
39	242.2	7.4	784	13	R3707166	R3707166	R3707166 U1-M-FRO-
40	239.6	7.4	815	12	BM548237	BM548237	BM548237 U1-M-EG0p
41	238.8	7.3	853	13	BU164703	BU164703	BU164703 AGENCOURT
42	234	7.2	558	9	A450906	A450906	A450906 ms26e01.x
43	232.6	7.2	315	13	BY363096	BY363096	BY363096 HY363096
44	228	7.0	926	13	BX327696	BX327696	BX327696 BX327696
45	227.8	7.0	475	9	AW082228	AW082228	AW082228 xb64c03.x

ALIGNMENTS

RESULT 1	U69184	U69184 Soares infant brain INIB Homo sapiens cDNA clonec 37299, mRNA	1114 bp	linear	EST 27-OCT-1999
DEFINITION	U69184	sequence.			
ACCESSION	U69184				
VERSION	U69184.1	GI:2739408			
KEYWORDS	EST.				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1114)				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	Sequencing analysis of forty-eight human image cDNA clones similar to drosophila mutant protein				
JOURNAL	DNA Seq. 9 (5-6), 307-315 (1998)				
MEDLINE	99452388				
PUBMED	10524757				
COMMENT	Contact: Zollo, Massimo Telethon Institute of Genetics and Medicine Via Olgettina 58, Milan, MI 20132, Italy Email: zollo@tigem.it.				
FEATURES	Location/Qualifiers				
source	1..1114				
	/organism="Homo sapiens"				

Db 181 GCACGATCCAAAGGCTTCAATGCAACCGCGCGCGAGCGCGCGCTGCTCTACCACTG 240

Qy 532 TCGGGGACCTGAGAGCAGCCCAAGGGCAAGCAAGCTCAATTAAGGGGTGTTGGG 591
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Qy 592 GAGAAACCAACTTGGCTGAGTCAAGAGTACCGGCGCATCGGAAGTGCCTTCATCCCTG 651
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AK048629 4015 bp mRNA linear HTC 05-DEC-2002
Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
library, clone: C130090D05 product: ELK CHANNEL 3 (FRAGMENT) homolog
(Rattus norvegicus), full insert sequence.

AK048629
VERSION AK048629.1 GI:26339459
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
PUBMED 10349636

REFERENCE
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374

11042159
3
REFERENCE
AUTHORS
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Todawa, Y., Izawa, M., Ohata, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multiplexed sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
PUBMED 11076861
4
REFERENCE
AUTHORS
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Aizawa, K., Iizawa, M., Nishi, K., Kiyosawa, H., Konno, S., Yamada, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, I., Saito, R.,
Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
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Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
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Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,
Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
King, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H.,
Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, I.,
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S.,
and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 585-590 (2001)
21085660
PUBMED 11217851
5
REFERENCE
AUTHORS
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 50,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4015)
REFERENCE
AUTHORS
Kawai, J., Aizawa, K., Akimura, T., Arawaka, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kadowa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, I., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohata, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takai, A., Akahira, S.,
Takeda, Y., Tanaka, J., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M., and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
COMMENT
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/

FEATURES

source

Location/Qualifiers

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NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 617)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Other_ESTs: 2820908.3prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DFP CDNA Library Preparation: Ling
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
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FEATURES
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California, Berkeley) using ZAP-cDNA synthesis kit
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ORIGIN

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QY 2911 CTCATGGACCTGGCCCTGGGTCCTCCCGCAGAGTCTCAGAGCTCCCTCCCTGGCTCCGCTCGAGCC 2970
 Db 483 CTCATGGACCTGGCCCTGGGTCCTCCCGCAGAGTCTCAGAGCTCCCTCCCTGGCTCCGCTCGAGCC 542
 QY 2971 ACAGCTTTCTGGACCTCCAGCTCAGACTCAGAGTCCCTGGCTCAGGAGAGCTCTGCTC 3030
 Db 543 ACAGCTTTCTGGACCTCCAGCTCAGACTCAGAGTCCCTGGCTCAGGAGAGCTCTGCTC 602
 QY 3031 GAGCCGACGACCCCT 3045
 Db 603 GAGCCGACGACCCCT 617

RESULT 8
 LOCUS CD354565
 DEFINITION UI-M-GMO-cgd-j-01-0-UI-r1 NIH-BMAP_GMC Mus musculus cDNA clone
 IMAGE: 30361272 5', mRNA sequence.
 CD354565
 CD354565.1 GI:31147066
 EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 704)
 NIH-MGC <http://mgc.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 CONTACT: Robert Strausberg, Ph.D.
 EMAIL: cgapbs-rsmall.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mouseefi.html>
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

Seq primer: pYX-5.
 Location/Qualifiers
 1..704
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE: 30361272"
 /tissue_type="whole brain"
 /dev_stage="1, 5 and 15 days newborn"
 /lab_host="JalOB (T1 phage resistant)"
 /clone_lib="NIH-BMAP-GMO"
 /note="Organ: Brain; Vector: pYX-Asc; Site: 1; EcoR I:
 Site 2: Not I; The library was constructed according
 Borado, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was size
 selected according to mRNA size fraction, ligated with EcoR
 I adaptor, digested with NotI and then cloned
 directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is CGAAGTGAAT. This library was created for the University
 of Iowa Brain Anatomy Project (BMAP). 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
 Program coordinator."

BASE COUNT 126 a 226 c 219 g 133 t
 ORIGIN

Query Match 17.9%; Score 582.4; DB 14; Length 704;
 Best Local Similarity 89.2%; Pred. No. 1.8e-99;
 Matches 628; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 1661 CCACGAGAGCTGCTCAGAGAGCTCCTGAGAGAGTCCGCGCAGAGATCCGATGACCTGC 1720
 Db 1 CCACGAGAGCTGCTCAGAGAGCTCCTGAGAGAGTCCGCGCAGAGATCCGATGACCTGC 60
 QY 1721 ACAAGAGAGCTCCTCAGAGTGCACCTGTTTGGAGGCGGCGCAGCGGGTCTGCTCGGGCAG 1780
 Db 61 ACAAGAGAGCTCCTCAGAGTGCACCTGTTTGGAGGCGGCGCAGCGGGTCTGCTCGGGCAG 120
 QY 1781 TGTCTCTGGCCCTGCGCGCCGCTTCTGACGCGCGGGAGTACTCATCCACCAAGGCG 1840
 Db 121 TGTCTCTGGCCCTGCGCGCCGCTTCTGACGCGCGGGAGTACTCATCCACCAAGGCG 180
 QY 1841 ATGCCCTCAGAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1900
 Db 181 ATGCTCTCAGAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 QY 1901 CGTCTCTGCCATCTAGGAGAGGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1960
 Db 241 CGTCTCTGCCATCTAGGAGAGGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 QY 1961 AGTGTGAAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2020
 Db 301 AGTGTGAAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 QY 2021 AGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2080
 Db 361 AGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 QY 2081 GTGGCTCGAGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2140
 Db 421 GTGGCTCGAGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 QY 2141 ACACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2200
 Db 481 ATACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 QY 2201 ATGGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2260
 Db 541 ATGGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
 QY 2261 TGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2320
 Db 601 TGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 QY 2321 CACCCCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2380
 Db 661 CGCTCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 704

RESULT 9
 LOCUS AL134774
 DEFINITION AL134774:2290_r1 547 (synonym: htfb1) Homo sapiens cDNA clone
 IMAGE: 30361272 5', mRNA sequence.
 AL134774
 AL134774.1 GI:6602961
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 651)
 Poustka, A., Wellenreuther, R., Mewes, H.W., Weil, B. and Wiemann, S.).
 EST (Poustka, A., Wellenreuther, R., Mewes, H.W., Weil, B. and Wiemann, S.).
 Unpublished
 CONTACT: Poustka A.J.
 Department Leirach
 Max-Planck-Institute for Molecular Genetics
 Ihnestr. 73, 14195 Berlin, Germany
 Tel: +49-30-84131623
 Fax: +49-30-84131128
 JOURNAL
 COMMENT

Email: poustka@camping-berlin-dahlem.mpg.de
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by DKFZ (German Cancer Research Center,
 Heidelberg/Germany) within the cDNA sequencing Consortium of the
 German Genome Project.
 No SL sequence available.
 This clone (DKFZp547I2290) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

source
 1..651
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZp547I2290"
 /tissue_type="brain"
 /dev_stage="fetal"
 /lab_host="Xl-2blue"
 /clone_lib="547 (synonym: hfbrl)"
 /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
 BASE COUNT 145 a 178 c 206 g 118 t 4 others
 ORIGIN

Query Match 16.9%; Score 550.6; DB 9; Length 651;
 Best Local Similarity 98.8%; Prod. No. 1.7e-93;
 Matches 553; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 272 AGGAGTCAAGCGTACGCTGATCCTGTACCGAGAGCGGGCTCCGCTTGTGGTCTCC 33;
 DB 1 AGGAGTCAAGCGTACGCTGATCCTGTACCGAGAGCGGGCTCCGCTTGTGGTCTCC 60
 QY 332 TGGATGTGATACCATGAAGAAAGGAGGAGTGCCTCTCTCTAGTCTCTCA 39;
 DB 61 TGGATGTGATACCATGAAGAAAGGAGGAGTGCCTCTCTCTAGTCTCTCA 120
 QY 392 AGGACATCAGCGAAACCAAGACGAGGGGCCCGGACAGATGGAAGACAGAGTGGTG 451
 DB 121 AGGACATCAGCGAAACCAAGACGAGGGGCCCGGACAGATGGAAGACAGAGTGGTG 180
 QY 452 GCCGGCGCGATATGGCGGCGACGATCCAAAGGCTTCATGCGACCGCGCGGAGGCC 511
 DB 181 GCCGGCGCGATATGGCGGCGACGATCCAAAGGCTTCATGCGACCGCGCGGAGGCC 240
 QY 512 GGGCGGTGCTTACCACTGTCCGGGACCTGCAGAGAGCGCCCAAGGCAAGCAAGC 571
 DB 241 GGGCGGTGCTTACCACTGTCCGGGACCTGCAGAGAGCGCCCAAGGCAAGCAAGC 300
 QY 572 TCATAAGGGGGTGTGGGGAGAAACCAACITGCTTGAGTACAAAGTAGCGGCATCC 631
 DB 301 TCAATAAGGGGGTGTGGGGAGAAACCAACITGCTTGAGTACAAAGTAGCGGCATCC 360
 QY 632 GGAAGTCCCTTCATCTGTTGCACTGTGGGCACTGAGAGCACTGGATGGATGCTCA 691
 DB 361 GGAAGTCCCTTCATCTGTTGCACTGTGGGCACTGAGAGCACTGGATGGATGCTCA 420
 QY 692 TCCTGCTGGCCACACTATATGTGGCTGTCACTGTGCCCTACAGCGTGTGTGAGCACAG 751
 DB 421 TCCTGCTGGCCACACTATATGTGGCTGTCACTGTGCCCTACAGCGTGTGTGAGCACAG 480
 QY 752 CACGGAGCCAGTGGCG 811
 DB 481 CACGGAGCCAGTGGCG 540
 QY 812 TCTTCATCTTGCAATGTG 831
 DB 541 TCTTCATCTTGTTACTGTG 560

RESULT 10
 AW249298
 LOCUS 501 bp mRNA linear EST 07-JAN-2000

DEFINITION 2821074.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821074 5',
 mRNA sequence.
 ACCESSION AW249298
 VERSION AW249298.1 GI:6592291
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 1 (bases 1 to 501)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Other_FEATURES: 282-074.3prime
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: DCTD/BTP cDNA Library Preparation: Ling
 Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
 Consortium (LLNL) DNA Sequencing by: Berkeley MGC Sequencing
 project Clone distribution: MGC clone distribution information can
 be found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.lnl.gov/dbp/image/image.html Base Calling / Quality
 Scores: PHRED from University of Washington Genome Center. Vector
 Trimming: cross_match from University of Washington Genome Center
 PARAP suite. Poly-T Identification: patMatch.pl from Berkeley
 Drosophila Genome Project. University of Washington Genome Center:
 http://www.genome.washington.edu
 Plate: LINC5 row: N column: 19
 High quality sequence stop: 500.
 Location/Qualifiers
 1..501
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2821074"
 /tissue_type="small cell carcinoma"
 /cell_line="MGC3"
 /clone_lib="NIH_MGC_7"
 /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(S). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript 1: RT (Life Technologies)."
 BASE COUNT 98 a 182 c 142 g 79 t
 ORIGIN

Query Match 15.1%; Score 452; DB 9; Length 501;
 Best Local Similarity 100.0%; Prod. No. 1.7e-82;
 Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1263 CAGCTCCGCCAGAGTGACAACTGCAGCAGCAGCAGCGGCGGCTGGA 1322
 DB 10 CAGCTCCGCCAGAGTGACAACTGCAGCAGCAGCAGCGGCGGCTGGA 69
 QY 1323 GCTGCTGGCGCGCGCTGCTGCGCAGCGCTTACATCACCTCCCTCTACTTCGCACCTCAG 1382
 DB 70 GCTGCTGGCGCGCGCTGCTGCGCAGCGCTTACATCACCTCCCTCTACTTCGCACCTCAG 129
 QY 1383 CAGCTCACCAGCGTGGGCTTGGGCAAGTGTGGCCCAACAGCAGCAGCAGAGATCTT 1442
 DB 130 CAGCTCACCAGCGTGGGCTTGGGCAAGTGTGGCCCAACAGCAGCAGCAGAGATCTT 189
 QY 1443 CTCATCTGCACCATGCTCATCGCGCGCTTGTCTGTACACAGCGCGCTGTTGGAGCGTAC 1502
 DB 190 CTCATCTGCACCATGCTCATCGCGCGCTTGTCTGTACACAGCGCGCTGTTGGAGCGTAC 249
 QY 1503 GGCATCATCCAGCGCATGTACGCCCGCGCTTCTGTACACAGCGCGCGCTTCTGTACACAGCGCGCGCT 1562
 DB 250 GGCATCATCCAGCGCATGTACGCCCGCGCTTCTGTACACAGCGCGCGCTTCTGTACACAGCGCGCGCT 309

Db 1 ATCTGAGCCAGGCTAGTAGATGCGCATTTGAAGCGGCTGTGGCTCGACAGCCCAAGT 60
QY TCCTCTTCGCGIGGGCCAGCTGSCCGGGAATGTAGCAGCAGCCCTCCCTCGACCA 2575
Db 61 TCTCTTTCCGCGTGGCCAGTCTGSCCGGAATGTAGCAGCAGCCCTCCCTCGACCA 120
QY AGAGCGGCTGCTCACTGTTCCCATGCGGCCAGCGAGGCAAGGAACACACACACTGG 2635
Db 121 AGAGCGGCTGCTCACTGTTCCCATGCGGCCAGCGAGGCAAGGAACACACACTGG 180
QY ACAGCTTCGCGAGCGGTGACAGAGTGTGACAGCAGGTGCTGCAAGTGGCGGAAGAC 2695
Db 181 ACAAGCTTCGCGAGCGGTGACAGAGTGTGACAGCAGGTGCTGCAAGTGGCGGAAGAC 240
QY TGCAGTCACTTCGCGAGCGGTGACAGTGTGCTGCGGCCAGCGAGGAGGTCC-GTGC 2754
Db 241 TGCAGTCACTTCGCGAGCGGTGACAGTGTGCTGCGGCCAGCGAGGAGGTCTGTGC 300
QY CTGCGGATCGGGAGAGGGCGGTGCCAGCCAGCAGCTCCGGCTTCGACGGCTTG 2814
Db 301 CTGCGGATCGGGAGAGGGCGGTGCCAGCCAGCAGCTCCGGCTTCGACGGCTTG 360
QY TGTGTGACACTGGGCACTCTCTACTGCTGACGCGCCAGCTGGCTCTGTCTGAGT 2874
Db 361 TGTGTGACACTGGGCACTCTCTACTGCTGACGCGCCAGCTGGCTCTGTCTGAGT 420
QY GGGACTTGGCCGCCACCTCGTCCGGGGCTCTCTCCCTCATGGCACCCGCGCTGGGT 2934
Db 421 GGGACTTGGCCGCCACCTCGTCCGGGGCTCTCTCCCTCATGGCACCCGCGCTGGGT 480
QY 2935 CC 2936
Db 481 CC 482

RESULT 13
A1272282 424 bp mRNA linear EST 18-NOV-1998
LOCUS ap23c04.x1 Schiller oligodendrogloma Homo sapiens cDNA clone
DEFINITION IMAGE:1956198.3' similar to IR:Q23974 Q23974 PUTATIVE POTASSIUM CHANNEL SUBUNIT 1, mRNA sequence.
ACCESSION A1272282
VERSION A1272282.1 GI:3894553
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
AUTHORS WashU-NCI human EST Project
JOURNAL Unpublished
COMMENT Contact: Wilson, R.K.
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco
High quality sequence stop: 401.
Location/Qualifiers
1. .424
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1956198"

/sex="male"
/tissue_type="oligodendrogloma"
/dev_stage="44 years"
/lab_host="SOLR"
/clone_lib="Schiller oligodendrogloma"
/note="Organ: brain; Vector: pBluescript SK- (Stratagene); Site 1: EcoRI; Site 2: XhoI; Double-stranded cDNA was prepared from human oligodendrogloma using primer 5'-GAGAGAGAGAGAGAGAACTAGTCTGAGT(18)-3'. An EcoRI adaptor was used on the 5' end of the cDNA as follows: 5'-AATTCGGCAGG-3'. The library was size-selected and sent through one round of amplification. Average insert size is 1.7 kb, with a range from 0.4-12 kb. Tumor identification by consensus pathology; contains chromosome 1p and 19q deletion as determined by CGH. This library was constructed by Dr. Martin Schiller (Johns Hopkins University)."
BASE COUNT 82 a 160 c 110 g 72 t
ORIGIN
Query Match 13.0%; Score 424; DB 9; Length 424;
Best Local Similarity 100.0%; Pred. No. 9.9e-70;
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1348 AGCGCTACATCACTCCCTCTACTTCGCACTCAGCAGCCTCACCAGCGTGGGCTTCGGC 1407
Db 1 AGCGCTACATCACTCCCTCTACTTCGCACTCAGCAGCCTCACCAGCGTGGGCTTCGGC 60
QY 1408 AACGTGCGGCCAACACGACCGACCGAAGATCTTCTGCACTCTGCACCATCTCATCGGC 1467
Db 61 AACGTGCGGCCAACACGACCGAAGATCTTCTCCATCTGCACCATCTCATCGGC 120
QY 1468 GCCTGATGACGCGGTGGTGTGGGAAGCTGACGCGCATCATCCAGCGCATGACGCC 1527
Db 121 GCCTGATGACGCGGTGGTGTGGGAAGCTGACGCGCATCATCCAGCGCATGACGCC 180
QY 1528 GCGCGCTTTGTGTACCAAGCGCACGCGCACTCTGCGGACATACATCCGATCCACCGT 1587
Db 131 GCGCGCTTTGTGTACCAAGCGCACGCGCACTCTGCGGACATACATCCGATCCACCGT 240
QY 1588 ATCCCCAAGCCCTCAAGCAGCGCATCTGGAGTACTTCCAGGCCACTGGGGGTGAAC 1647
Db 241 ATCCCCAAGCCCTCAAGCAGCGCATCTGGAGTACTTCCAGGCCACTGGGGGTGAAC 300
QY 1648 AATGGCATGACACACCGAGCTGCTGCAGAGCTCTGCTGACGAGTCTGCGCGAGAGATC 1707
Db 301 AATGGCATGACACACCGAGCTGCTGCAGAGCTCTGCTGACGAGTCTGCGCGAGAGATC 360
QY 1708 GCCATGACCTGCAAGAGAGGTCTGCACTGCTGCTGCTTTGAGGCGGCCAGCGCGGC 1767
Db 361 GCCATGACCTGCAAGAGAGGTCTGCACTGCTGCTGCTTTGAGGCGGCCAGCGCGGC 420
QY 1768 TGCC 1771
Db 421 TGCC 424
RESULT 14
B0444229 682 bp mRNA linear EST 29-MAY-2002
LOCUS UI-M-EX0-bxk-c-05-0-UI.r1 NIH-BMAP_EX0 Mus musculus cDNA clone
DEFINITION IMAGE:5709244.5', mRNA sequence.
ACCESSION B0444229
VERSION B0444229.1 GI:21247341
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 682)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: rstrasb@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: XGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pyX-5.
Location/Qualifiers
1. 682

FEATURES

source

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:570924"
/tissue_type="whole brain"
/dev_stage="embryo 15.5 dpc"
/lab_host="bH10B (T1 phage resistant)"
/clone_lib="NIH-BMAP-EX0"

/note="Organ: Brain; Vector: pyX-Asc; Site_1: EcoR 1;
Site_2: Not I; The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:75-80,
1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pyX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is GTCCGTGGA. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institutes of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."
128 a 205 c 202 g 147 t

BASE COUNT
ORIGIN

Query Match 11.4%; Score 369.8; DB 13; Length 582;
Best Local Similarity 78.4%; Pred. No. 1.7e-59;
Matches 443; Conservative 0; Mismatches 122; Indels 0; Gaps 0;
QY 1330 GCGCGCGCTGCTCGCGAGCGCTACATACCTCCCTCTACTTCGCACACGAGCGTC 1389
DB 103 GTGACCATCTCGCGCAGTGCGCTACATCGCTGGCTGTACTTCACGCTGAGCGCTC 162
QY 1390 ACCAGCGTGGCTTCGGCAAGCTGTCCGCCAACAGCGGACCGGACAGATCTTCCTCATC 1449
DB 163 ACCAGTGTAGGCTTCGGCAAGCTGTGTGCCAACACAGACGCTGAGAAGATCTTCCTCATC 222
QY 1450 TGCACCATCTCATCGCGCCCTGATGCACGCGTGTGTGTGGAGCGTGACGCCCATC 1509
DB 223 TCACGATGCTCATAGGCGCGCTGATGCACGAGTGTGTGTGGATGTGCACAGCATC 282
QY 1510 ATCCAGCGCATGTAGCGCGCGCTTCTGTACACAGCCAGCGCGACCTCGCGGAC 1569
DB 283 ATCCAGCGCATGTACTCCGACGCTCGCTACACAGCCGCGCATGAGGATCTCAAGGAC 342
QY 1570 TACATCCGATCCACCGTATCCCAAGCCCTCAGCAGCGCATGCTGGAGTACTTCAG 1629
DB 343 TACATCCGAGTGCATCGCGCTGCCCGCCCACTCAAGCAGCGCATGCTCGACTTCAG 402
QY 1630 GCACCTGGCGGTGAACAATGGCATTCGACACACCGAGCTGCTGCAGAGCTCCCTGAC 1689
DB 403 AGCAGTGGCGAGTCAACAGCGCATCGATGCCACAGAGTACTGCGGTGACTTCCGAT 462
QY 1690 GAGCTGGCGGACATCGCCATGCAACCTGCACAGAGAGTCTCTGACACTGCCACTTTT 1749
DB 463 GAGTGGCTGCTGACATTCTATGCACCTGAAACAGGAGATCTCTGCAGCTGCCTCTGTT 522

QY 1750 GAGCGCGCAGCGCGGCTGCTCGGGCACTGTCTCTGCGCGCGCGCGCTTCTGCG 1809
DB 523 GAGCGCGTACGAGGCGTCTCGGGCCCTCTCTTGACATCAAGACCTCTCTTCTG 582
QY 1810 ACGCCGCGGAGTACCTCATCCACAAAGGCGACCTCGCGAGGCGCTCTACTTGTCTG 1869
DB 583 GCTCTGGGAGTACCTGTACGCGGTGGGATGCTCCCTCCAGGACACACTACTAGCTCTG 642
QY 1870 TCTGCTCCATGGAGGCTCAAG 1894
DB 643 TCTGCTCGCTGAGGTGCTCCGG 667

RESULT 15

B1975332

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PubMed

COMMENT

FEATURES

source

Location/Qualifiers

/organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"

/tissue_type="pooled"

/lab_host="DH10B"

/clone_lib="MARC 2BOV"

/note="Vector: pCMV SPOT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from testis, thymus,
semitendinosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

Length

DB 12;

Pred. No. 7.3e-58;

Matches

412;

Conservative

0;

Mismatches

45;

Indels

4;

Gaps

2;

QY 2752

CCTCCGGGCTTCGACGCTCTGTGTGGACACTGGGCGATCTCTCTACTGCGGACG 2851

DB 4

CCTCTGGGCTGTGACGCGCTGTGTGTGGACACTGGGCGATCTCTCTCTCTCTCTCT 63

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QY 2852 CCCAGCTGGCTGTGTCTGAGTGGGACTTGGCCCAACCCCTGCTCGGGGGCCTCGTCGCC 2911
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
64 CCTCAGCTGGCTGTGTCTGAGTGGGACTTGGCCCAACCCCTGCTCGGGGGCCTCGTCGCC 123
QY 2912 TCATGGCACCCCTGGGCGCTGGGTCGCCCCAGCGCTCTCAGAGCTCCCCCTGGGCTCAGGCA 2971
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
124 TCATGGCTCCCTGGGCGCTGGGCGCGCCCTGCATCTCAGAGCTCAGCATGGGCTCAGGCA 183
QY 2972 CAGCTTCTGGACCTCCAGCTCAGACTCAGAGCGCCCTGCCCTCAGGAGACTCTGCTCTG 3031
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
184 CTGCTTTTGGACCTCCAGCTCTGACTCGGAGCGCCCAAGGCTCAGGAGAACTCTGCCCTG 243
QY 3032 AGCCAGCACCCCTGGCTCCCTCTCTCTGAGGAGGGGCTAGGACTGGGCGCCCGCAG 3091
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
244 AGCCAGCACCCCTGGCTTACCGCTC--CCGAGGAGGGGCTAGGACTGGGCGCCCGG 300
QY 3092 AGCCTGTAGCCAGGCTGAGGCTACCAGCACTGGAGAGCCCCCACAGGGTCAGGGGSCC 3151
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
301 AGCCCATGACCCAGGCTGAGGCTGCCAGCACCGGAGGCCGCCACAGCTTCGGGGGGCC 360
QY 3152 TGGCCTTGCCCTGGGACCCGCCACAGCCTGGAGATGCTTATGSGCTGCCATGCTCTG 3211
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
361 ACGCCITGCCCTGGAGCCCCATAGCCTGGAGATGCTTATCGGCTGCCACGGCTCTG 420
QY 3212 GCACAGTCCAGTGGACCCAGGAGAACAGGCAAGGGGTCTGA 3252
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
421 GTACAGTCCAGTGGACCCAGGAGAA-GCACAGGGGTCTGA 460
```

Search completed: October 1, 2003, 21:12:57
Job time : 5973 secs